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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen
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P50592 mus musculu
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8 macropus eu
3 ovis aries
4 macaca mula
0 papio hamad
2 canis famil
7 macaca fasc
                                                                                                                                                                                                                                           4 oryctolagus
5 sus scrofa
5 cavia porce
3 sus scrofa
9 peromyscus
8 mus musculu
10 bos taurus
11 sequus cabal
14 marmota mon
15 homo sapien
16 canis famil
18 cervus elapj
19 homo sapien
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18 cervus elapj
18 homo sapien
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3 homo sapien
0 rattus norv
7 homo sapien
9 bos taurus
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36 113.5 11.4 233 1 TNFA_TRIVU 37 111.5 11.2 233 1 TNFA_TRIVU 38 111.5 11.2 202 1 TNFB_RAT 38 111.5 11.2 302 1 TNFB_RAT 38 111.5 11.1 391 1 EDA_MOUSE 39 108.5 10.9 306 1 TNFC_MOUSE 40 108 10.8 193 1 TNFA_CACHI 41 108 10.8 233 1 TNFA_MACEU 42 107 10.7 197 1 TNFB_RASIT 43 106 10.6 391 1 EDA_HUMAN 44 102 10.2 244 1 TNFC_HUMAN 45 98.5 9.9 233 1 TNFA_FELCA AC P50591 1 EDA_HUMAN 45 98.5 9.9 233 1 TNFA_FELCA AC P50591 1 TOOT-1996 (Rel. 34, Created) DT 01-CCT-1996 (Rel. 34, Last sequence update) DT 01-CCT-2900 (Rel. 34, Last sequence update)	
113.5 11.4 233 111.5 11.2 202 111.1 11.1 391 108.5 10.9 306 108.5 10.9 309 108 10.8 133 107 10.7 197 106 10.6 391 107 10.7 197 106 10.6 391 102 10.2 244 98.5 9.9 233 98.5 9.9	ω, ω
11.4 233 11.2 233 11.2 203 11.2 203 11.2 203 11.9 306 10.8 133 10.8 233 10.7 197 10.6 391 10.6 391 10.2 244 9.9 233 9.	
233 203 203 203 203 203 203 203 203 203	<u>. i-</u>
33 1 TNF 33 1 TNF 33 1 TNF 34 1 TNF 35 1 TNF 37 1 TNF 37 1 TNF 38 1 TNF 39	
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TWFA_TRIVU TNFA_BOVIN TNFA_BOVIN TNFA_ROTIN TNFA_MOUSE TNFA_CAPHI TNFA_CAPHI TNFA_MACEU TNFB_RABIT EDA_HUMAN TNFA_FELCA ALIGNMENTS ALIGN	OUSE
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Best I
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                                       Cytokine;
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P50592;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER
                                                                          PROSITE;
                                                                                                                                   EMBL;
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINB=96111955; PubMed=8777713;

Wiley S.R., Schooley K., Smolak P
Nicholl J.K., Sutherland G.R., Da
Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TN10_MOUSE
                             DOMAIN
                                                                                                                                                                                                                                                                                                               "Identification and characterization family that induces apoptosis."; Immunity 3:673-682(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APOPTOSIS INDUCING LIGAND) THESF10 OR TRAIL.
                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                  SUBUNIT: HOMOTRIMER (POTENTIAL).
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN
TISSUE SPECIFICITY: WIDESPREAD.
                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                      FUNCTION: INDUCES APOPTOSIS
                                                                                                                          MGI:107414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EASFFGAFLVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRK 150
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                                                                                                   PF00229;
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                                                                         PS00251; TNF_1; PS50049; TNF_2;
                            ; Transmembrane;
1 17
18 38
39 291
                                                                                                              IPR000478;
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39
281
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                                                                                                                                     AAC52345.1; -.
                                                                                                   TNF;
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281
32509
1; 1.
2; 1.
2; 1.
ne; Signal-anchor; Apoptosis.
ne; CYTOPLASMIC (POTENTIAL).
38 SIGNAL-ANCHOR (TYPE-II MEMBR.
31 EXTRACELLULAR (POTENTIAL).
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Pred. No. 1.1
); Mismatches
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EXTRACELLULAR (POTENTIAL).
DDAAAF78DAAB2F6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                               k P.J., Din W.S.,
Davis-Smith T.,
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No. 1.
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.s 0;
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                                                                                                                                                                                                                                                                               (POTENTIAL).
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                                       MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae;
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                                       PROTEIN)
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Best Local s
Matches 134
                                                                                                                                                                                                                                                                                                                                                                                                                                               TNIL MOUSE STANDARD;

035235; 035306;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR LIGAND SUPERPAMILY MEMBER 11 (RECEPTOR ACTIVATOR OF NUCLEAR FACTOR KAPPA B LIGAND) (TRANKL) (TWP-RELATED ACTIVATION-INDUCED CYTOKINE) (TRANCE) (OSTEOPROTEGERIN LIGAND) (OPGL) (OSTEOCLAST
                                                                                                                                                                                                                                                                                                   SEQUENCE ....
TISSUE=Hybridoma;
MEDLINE=97460112; PubMed=9312132;
Mong B.R., Rho J., Arron J., Robinson E.,
Wong Y. S., Cayani E., Bartlett F.S. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
SEQUENCE
                                                                                                          "Osteoprotegerin ligand is differentiation and activat Cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
       Yasuda H., Shima N., Nakagawa N., Yamaguchi K.,
Mochizuki S.-I., Tomoyasu A., Yano K., Goto M.,
Morinaga T., Higashio K., Udagawa N., Takahashi
"Osteoclast differentiation factor is a ligand
                                                                                                                                                            Lacey D.L., Timms E., Tan H.-L., Kelley M.J.,
Burgess T., Elliott R., Colombero A., Elliott
Sullivan J., Hawkins N., Davy E., Capparelli C
Kaufman S., Sarosi I., Shalhoub V., Senaldi G.
                                                                                                                                                                                                            rissue=Bone marrow;
MEDLINE=98227661; P
                                                          TISSUE=Bone marrow stroma;
MEDLINE=98188248; PubMed=9520411;
                                                                                                                                                                                                                                                                "TRANCE is a novel ligand of the tumor that activates c-Jun N-terminal kinase J. Biol. Chem. 272:25190-25194(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                   Boyle W.J.;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWESSRKGHSFLNHVLFRNGELVIEQEGLYYIYSQTYFRFQEAEDASKMVSKDKVRTKQL
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134; Conser
                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                             OR TRANCE
                                                                                                                                                                                                                PubMed=9568710;
                                                                                                                        gand is a cytokine that regulates
  activation.";
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33477
                                                                                                                                                                                                                                                                                                                                                                                                         Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
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Pred.
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; 3FEACAB9F0D7D802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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No. 1.
                                                                                                                                                                                                                                                                             necrosis factor receptor family
in T cells.";
                                                                                                                                                                                                                                                                                                                 III, Franke
                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata;
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.3e-52;
                                                                                                                                                                G.,
                                                                                                                                                                                                                                                                                                                                                                                                         Muridae;
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                                                                                                                                                                                                                                                                                                                   Frankel
                                                                                                                                                                         Dunstan C.R.,
G., Scully S., Hsu
C., Eli A., Qian Y.
factor
         for
                   Kinosaki
Murakami
N., Suda
                                                                                                                                                               Guo J.,
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and
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                                                                                                                                       osteoclast
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.N., I
                                                                                                                                                               Delaney
                      H > X
ST
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                                   Tsuda
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                                                                                                                                                                J.,
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QΥ
                                                                                                           Query Match
Best Local S
Matches 65
                                                                                                         CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       EMBL; AF053713; AAC40113.1; -. EMBL; AF013170; AAC71061.1; -. EMBL; AB008426; BAA25425.1; -. EMBL; AF019048; AAB86812.1; -. EMBL; AB036798; BAA97259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-Thymic lymphoma;
TISSUE-Thymic lymphoma;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Do
Anderson M.E., Roux E.R., Teepe M.C., DuBose R.F.,
                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1100089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                                        CARBOHYD
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                   Cytokine;
                                                                                                                                                                                                                                                                                                               InterPro; IPR003263;
                                                                                                                                                                                                                                                                                                                             InterPro; IPR000478; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to TRANCE/RANKL.";
                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                    ignal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN T CELLS.
TRABECULAR BONE ADD LUNG.

DISEASE: DEFICIENCY IN THEST11 RESULTS IN FAILURE TO FORM LOBULO-ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA, WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN HYPERTROPHIC CHONDROCYTES.
 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homologue of the TNF receptor and its ligand enhance T-cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL). TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR. AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
SEETI--
                                               Similarity
                                                                                                                                                                                                                                                                 PS00251; TNF_1; FALSE_NEG PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                 Differentiation;
                                                                                                      99
316
                                                                                                                                      70
197
262
                                Conservative
                                                                                                                                                                                                     49
                                                                                                                                                                                                                                                                                                  TNF; 1
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                                                                                                  316
197
262
99
34944
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                                                                                                                                                                                                     48
69
                                               23.6%;
-STVQEKQQNISPLVRERGPQRVA-
                                                                                                            ¥.
                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .A. 95:3597-3602(1998)
                                                                                                                                                                                                                                                   Receptor; Glycoprotein; Transmembrane;
                         Pred. No. 3e-17; Mismatches
                                                                                                                      (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
G -> D (IN REF. 4).
                                               Score 235.5;
Pred. No. 3e
                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL) SIGNAL-ANCHOR (TYPE II
                                                                                                         -> D (IN REF. 4).
08DF63A2BE00967A CRC64;
                                               3e-13;
                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dougall W.C.,
                                                                                                                                                                                                     II MEMBRANE PROTEIN)
                                                          Length
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cosman D.,
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                                                             316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
                              53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
                              Gaps
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RESULT
TN11_H
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7111_HUMAN STANDARD; PRT; 317 AA.

7114788; 014773; 09P2Q3;

101-0CT-2000 (Rel. 40, Last sequence update)

101-0CT-2000 (Rel. 40, Last annotation update)

710-0CT-2000 (Rel. 40, Last sequence update)

71
                                                                                                                                                                                                                                                                                                                       TISSUE=Thymocytes;
MEDLINE=97460112; PubMed=9312132;
Wong B.R., Rho J., Arron J., Robinson E.
Kalachikov S., Cayani E., Bartlett F.S.
                                             "Cancer cells responsible for encoding a secreted form of formation.";
                                                                                                                                                                                                                                                                   that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Osteoprotegerin ligand is differentiation and activation and stivation and stivation and stivation (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu Sullivan J., Hawkins N., Davy E., Capparelli C., Ell A., Qian Y.-Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lymph node;
MEDLINE=98227661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson D.M., Maraskovsky E., Billingsley W. Tometsko M.E., Roux E.R., Teepe M.C., DuBose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Bone marrow, and Peripheral blood, MEDLINE-98032977; PubMed-9367155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFSF11 OR RANKL OR TRANCE OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                         Biochem.
                                                                                                                                          MEDLINE=20175237;
                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 73-317 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boyle W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                   TISSUE=Tongue;
                                                                                                                                                                                                                                                                                         TRANCE is a novel ligand of the tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 FYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211
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                                                                                                                                                                                                                                         Biol.
  FUNCTION:
                                                                                                                                                                                                                                                                   activates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFH 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEDTLPDSCRRMKQAFQGAVQKELQHIV-----GPQRFSGAPAMMEGSWLDVAQRGKPE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK 89
                         Biophys.
                                                                                                                                                                                                                                         Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         node;
                                                                                                                                                                                          N.A. (ISOFORM
OSTEOCLAST DIFFERENTIATION AND
                                                                                                                                                                                                                                    c-Jun N-terminal kinas
272:25190-25194(1997).
                                                                                                                                            PubMed=10708588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9568710;
                         Res.
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                           Commun.
                                                                                               Sato N.;
le for humoral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPGL
                         269:532-536(2000)
                                                                   hypercalcemia
E that induces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulates osteoclast
                                                                                                                                                                                                                                                                   cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .L., Dougall W.C., R.F., Cosman D.,
ACTIVATION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312
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                                                                                               express mRNA
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                                                                        osteoclast
                                                                                                                                                                                                                                                                                                                                         Lee
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FASL_MOUSE
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Best Local S
Matches 52
       FASL_MOUSE STANDARD; PRT; 2:
P41047; Q61217; Q9R1F2;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up:
01-OCT-2000 (Rel. 40, Last annotation
FAS ANTIGEN LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF019047; AAB86811.1; -. EMBL; AF053712; AAC39731.1; -. EMBL; AF013171; AAC51762.1; -. EMBL; AB037599; BAA90488.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000478; -.
                                                                                                                                                                276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTÉS, BONE MARROW PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROTD. INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION. SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECRETED (ISOFORM 2).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SOI
PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL PROLIEBRATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL HYPERCALCEMIA OF MALIGNANCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
                                                                                                                                                                                                                                                                                                          AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602642; -
                                                                                                                                                                NVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                          YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 190
                                                                                                                                                                                                                        LYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSI
                                                                                                                                                                                                                                                    IYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSI 152
                                                                                                                                                                                                                                                                                 AHLT-----INATDIPSGSHKVSL----SSWYHDR-GWAKISNMTFSNGKLIVNQDGFYY
   ဝ္ဂ
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00251; TNF_1; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                 194
317
                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
171
198
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative
OR FASL OR
                                                                                                                                                                                                                                                                                                                                                                                                                   194
35478
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Pred.
   GLD
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N-LINKED (GLCNAC. . .) (F
N-LINKED (GLCNAC. . .) (F
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-> G (IN REF. 3).
766176446348097F CRC64;
                                                                                                                                                                                                                                                                                                                                          Mismatches
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No. 5.4
                                            update)
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OR (TYPE II MEMBRANE PROTEIN)
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HEART,
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-i- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED I
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C3H; TISSUE=Spleen;
MEDLINE=20021694; PubMed=10552956;
Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
"Cloning and expression of a short Fas ligand: A new alternspliced product of the mouse Fas ligand gene.";
                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION OF VARIANT GLD MEDLINE-96091792; PubMed-749574!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNF family gene cluster.";
Immunity 1:131-136(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lynch D.H., Watson M.L., Alderson M.R., Baum
Tough T., Gibson M., Davis-Smith T., Smith C.
"The mouse Fas-ligand gene is mutated in gld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM FASL).
MEDLINE=95196085; PubMed=7889405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6;
MEDLINE=95388076; PubMed=7544870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Generalized lymphoproliferative mutation in the Fas ligand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM FASL). MEDLINE=94185175; PubMed=7511063;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 two amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peitsch M.J., Tschopp J.J.;
"Comparative molecular modelling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell 76:969-976(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi T., Tanaka M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mus musculus Balb/c
two amino acids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fenner M.H., Shioda T., Isselbacher K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                          INTERACTION.

DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
              European Bioinformatics Institute.
                                                                                                                                                  ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTO: WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
                                                                                                                                                                                                                 SUBUNIT: HOMOTRIMER (PROBABLE)
SUBCELLULAR LOCATION: ISOFORM I
                                                                                                                                                                                                                                                         CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT. FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
                                                                                                                                                                                                ISOFORM FASLS IS SOLUBLE.
                                                                                                                                                                                                                                            T CELLS, OR BOTH
                         SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunol. 32:761-772(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                              94:3456-3467(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         etazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                PubMed=7495745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORM FASL),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORM FASLS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brannan
                                                                                                                                                                                                              ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differs from 129/SV Fas ligand
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            There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fas-ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in
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A., Hunter K.;
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            restrictions on
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                              EMBL outstation
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                                          collaboration
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Best Local
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VARSPLIC
                                                                                 FASL_HUMAN STANDARD; PRT; 281 AA. P48023; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) FAS ANTIGEN LIGAND) FASS ANTIGEN LIGAND THESE OR APTILG1 OR FASL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
VARIANT
           SEQUENCE FROM N.A. MEDLINE-95105731;
                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not remove
entities requires a license agreement (So
or send an email to license@isb-sib.ch).
                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                     GTALISGVKYKKGGLVINETGLYFVYSKVYFRGQ-----SCNNQPLNHKVYMRNSKYPE
                                                                                                                                                                                                                                                                                                         GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYPD
                                                                                                                                                                                                                                                                                                                             VSSFEKQIANPSTPSEKKEPRSV-AHLTG------NPHSRSIPL-----EWEDT-Y 164
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                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation;
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PS50049; TNF_2;
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             PubMed=7528780
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2248,
2184
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                                                     Chordata;
Primates;
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27.1%;
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Glycoprotein; Signal-anchor; Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN ISOFORM FASLS)
T -> A (IN STRAIN BALB/C).
E -> G (IN STRAIN BALB/C).
F -> L (IN GLD; ABOLISHES
TO ITS RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                      Score 188.5; DB 1;
Pred. No. 2.8e-09;
6; Mismatches 59;
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Splicing.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANGER (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
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                                                    Craniata; Vo
Catarrhini;
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ED (GLCNAC...) (POTE)
ED (GLCNAC...) (POTE)
ED (GLCNAC...) (POTE)
G (IN ISOFORM FASLS).
                                                                Vertebrata; Euteleostomi;
                                                     Hominidae;
                                                                                             (APTL).
                                                                                                                                                                                                                                                                                                                                                                                          Length
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(POTENTIAL).
(POTENTIAL).
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MALSUMULA M., Nakanishi Y., Ohba Y.;
Matsumula M., Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.

FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
 DOMAIN
DOMAIN
DOMAIN
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                     PROSITE; Cytokine;
                                                                                                                                                                        EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human Fas ligand: gene structure, specificity."; Int. Immunol. 6:1567-1574(1994).
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MEDLINE-95127560; Pubmed-7826947;
Tanaka M., Inazawa
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                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
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Mita E., Hayashi N.,
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SUBUNIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE II M
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U08137; AAC50071.1;

U11821; AAC50124.1;

U11822; BAA07320.1;

D38122; BAA07320.1;

CAB09424.1;
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Glycoprotein; Signal-anchor; Apoptosis.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94084792; PubMed-7505205;
Suda T., Takahashi T., Golstein P., Nagata S.;
"Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family.";
Cell 75:1169-1178(1993).
-I- FUNCTION: CYPORKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FASS ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PASIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
                                                    InterPro; IPR000478; -
Pfam; PF00229; TNF; 1.
                                                                                                                                                               the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia;
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T CELLS, OR BOTH.

SUBUNIT: HOMOTRIMER (PROBABLE).

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY

SUBCELLULAR FLUID, PROBABLY BY CLEAVAGE F
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INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
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TN14_HUMAN
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Best Local
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DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=98122340; PubMed=9462508;

Mauri D.N., Ebner R., Montgomery R.I., Ko

Mauri D.N., Ebner R., Murphy M., Eisenberg
                                                                                                                                                                                                                                                                                                                                                                                                                     TN14_HUMAN STANDARD; PRT; 240 AA.
043557; 075476;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytokine;
DOMAIN
                                                   growth.";
J. Biol. Chem.
                                                                               HVEM/TR2,
                                                                                                                  Tan K.B., Dede K., Spampanato J., Silverman DiPrinzio R., Emery J.G., Deen K., Eichman C
                                                                                                                                                                                                              "LIGHT, a new member of ligands for herpesvirus immunity 8:21-30(1998).
                                                                                                                                                                                                                                                                                                                                                                                   MEDIATOR-LIGAND) (HVEM-L).
TNFSF14 OR LIGHT OR HVEML.
                                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR LIGAND MEDIATOR-LIGAND) (HVEM-L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                        <del>-</del>
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                          TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                            Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D.,
                                                                                                                                                           MEDLINE=98438532; PubMed=9765287;
                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                             Herpesvirus entry mediator ligand IVEM/TR2, stimulates proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 LY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
FUNCTION: ACTIVATES NPKB, STIMULATES THE PROLIFERATION OF T CELLS, AND INHIBITS GROWTH OF THE ADENOCARCINOMA HT-29. ENGAGES THE RECEPTOR FOR THE LYMPHOTOXIN-ALPHA-BETA HETEROTEXHER BUT DOES NOT FORM COMPLEXES WITH EITHER LT-ALPHA OR LT-BETA. ACTS AS A RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISTVQEKQQNISPLVRERGPQRVAAHITGT-RGRSNTLSSPNSKNEKALGRKINSWESSR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSSFEKQIANPSTPSETKKPRSV-AHLTGNPRSRSIPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDLVLMEEKKLNYCTT--GQIWAHSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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100 278
4
69
45 58
199 230
116 116
247 247
257 257
278 AA; 31140 P
                                                                                                       Young P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                     273:27548-27556(1998)
                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.8%;
27.5%;
                                                                                                                                                                                                                              the TNF superfamily, and entry mediator.";
                                                                                                                                                                                                                           entry mediator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-PRO.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (PO:
                                                                                                                                                                                                                                                                                                                                                                                                             SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN). EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyTopLasmIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO-RICH
                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                               Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                             (HVEM-L), a novel ligand of T cells and inhibits F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177.5;
                                                                                                                                                                                                                                                                              Kochel K.D., Cheung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5e-08
                                                                                                                                                                                                                                                                 R.J.,
                                                                                                                                                                                                                                                                                                                                               Hominidae;
                                                                                                                    C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                 c.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCNSQPLSHKVYMRNFKYP
                                                                                                                                                                                                                                                                   Cohen
                                                                                                                     Chabot-Fletcher M.,
                                                                                                                                                                                                                                                                                                                                                                                                             14 (HERPESVIRUS
                                                                                                                                   Hensley
                                                                                                                                                                                                                                         lymphotoxin alpha are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EWEDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                   G.H.,
                                                                                                                                             Minton
                                                                               d for
HT29
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                                                                                                                                                                                                                                                                   Spear P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                cell
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OCC COC DT DT AC
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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Best Local S
Matches 50
                                                                                                                                                                                                                                                 01-OCT-1996
01-OCT-1996
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the provided by a support of the statement is not removed.
                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
                                                                                                                                                                                                                                                                                                                                                                                                                 BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                         TNFSF5 OR CD40LG
                                                                                                                                                                                                                    CD40 LIGAND
                                                                                                                                                                                                                                                                                                                                                P51749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine; Cytotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00251; TNF_1; FALSE_NEG PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                             rnf5_bovin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 TRSYFGAFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 LVRERGPORV--AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION. SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR NONHEMATOPOIETIC TUMOR LINES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR HERPES SIMPLEX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EASFFGAFLV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SYPDPILLMKSARNSCWSKDAEYGLY--SIYQGGIFELKENDRIFYSYTNEHLIDM-DH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGALVVTKAGYYYIYSK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRYPEELELLVSQQSPCGRATSSSRVWWDSSFLGGVVHLEAGEEVVVRVLDERLVRLRDG
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6 (Rel. 34, Last
7) (Rel. 39, Last
7) (TNF-RELATED 1
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214
240
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                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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AAC25169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                         OR CD40L.
                                                                                                                                                                                                                                              . 34, Created)
. 34, Last sequence and the sequence and t
                                Bos.
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102
214
26351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Glycoprotein; Signal-anchor.
37 CYTOPLASMIC (POTENTIAL).
58 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.3%;
                                                                                                                                                                                                                    ast sequence up
ast annotation
D ACTIVATION PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL)

E -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 152; DB 1;
Pred. No. 3.2e-06;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49D0BF67E1390B39
                                                                                                                                                                                                          on update)
PROTEIN) (TRAP) (T CELL ANTIGEN
                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                             261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IYKYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFA_RABIT
                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                          13-AUG-1987 (Rel. 05, 0
13-AUG-1987 (Rel. 05, 1
15-JUL-1999 (Rel. 38, 1
TUMOR NECROSIS FACTOR P
TNF OR TNFA.
                                                                                                                                                TNFA_RABIT
P04924;
13-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A MEDLINE=91065534;
                                        NCBI_TaxID=9986
                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z48469; CAA88363.1; HSSP; P29965; 1ALY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00229; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenetics 42:430-431(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mertens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96006582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                           130
                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                     147
                                                                                                                                                                                                                                                                                                                                                          104
                                                                                                                                                                                                                                                                                                                               73
                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor alpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF INVOLVED IN IMMUNOCLOBULIN CLASS SWITCHING (BY SIMILAR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                RILLRAANTHSSSKPC--GQQSIHLGGVFELQSGASVFVNVTDPSQVSHGTGFTSFG
                                                                                                                                                                                                                                                                                                    TLSNNLVTLENGKQLAVKRQGFYYIYTQVTFCSNRE----TLSQAPFIASLCLKSPSGSE 202
                                                                                                                                                                                                                                                                                                                 FLSN--LHLRNG-ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDP 129
                                                                                                                                                                                                                                                                                                                                                                                    VQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS 72
                                                                                                                                                                                                                                                                          ILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
                                                                                                                                                                                                                                                                                                                                                          VKKKEKNFEMHKGDQEPQ-IAAHV------ISEASSKTTSVL-----QW--APKGYY 146
                                                                                                                                                                                                                                                                                                                                                                                                               49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00251; TNF_1;
; PS50049; TNF_2;
; PS50049; TNF_2;
; e; Transmembrane;
1
2
2
M 23 46
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000478; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47
178
240
261
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A.
                                                                                                                                                                             STANDARD;
 PubMed=2249779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muriuki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7590981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261
218
240
29242
                                                     Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%;
27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         i; 1.
2; 1.
2; 1.
ie; Glycoprotein; Signal-anchor.
2 CYTOPLASMIC (POTENTIAL).
5 SIGNAL-ANCHOR (TYPE-II ME)
6 'POTENTIAL). 'POTENTIAL)
                                                                                                       Last sequence update)
Last annotation update)
PRECURSOR (TNF-ALPHA) (CACHECTIN)
                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X
W
Y
                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 142; DB
Pred. No. 2.6e-
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaidulis
                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·LINKED (GLCNAC. . .) (F
8491FEFB30A787FD CRC64;
                                                     Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                         142; DB 1;
No. 2.6e-05;
                                                                                                                                                                             235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no rest
ng as its content
                                                      Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXISTS
                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN)
                                                                                                                                                                                                                                                257
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Query Match
Best Local S
Matches 42
                                                                                                      DISULFID
CONFLICT
SEQUENCE
                                                                                                                                                                                                                     InterPro; IPR000478; ...
InterPro; IPR002959; ...
Pfam; PF00229; TWP; 1.
PRINTS; PR01234; TMECROSISFCT.
PRINTS; PR01235; TMFALPHA.
PROSITE; PS00251; TMF_1; 1.
PROSITE; PS00251; TMF_2; 1.
Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihar Hayashi H., Kato M., Seko M.;
"Molecular cloning and expression in Escherichia col coding for rabbit tumor necrosis factor.";
DNA 5:149-156(1986).
-I- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES,
                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor.";
DNA 5:157-165(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-86219712; PubMed-3519138; Ito H., Shirai T., Yamamoto S., Akira M.,
                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=86219711; PubMed=3519137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wallace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 95:215-221(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural
                                                                                                                                                                                                                                                                                                                                                                                                   BL; M12845; AAA31486.1; -.
BL; M12846; AAA31482.1; -.
BL; M60340; AAA31484.1; -.
R; A25451; A25451.
R; A25454; A25454.
R; J80727; J807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE
SUBCELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKI MITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUNOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: CACHEXIA ACCOMPANIES A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CANCER AND INFECTION, AND AND MALNUTRITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEOLYTIC PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE SOLUBLE FORM DERIVES
                                                                                                    148
63
235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analysis
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuprash D.V.,
                                                                                                        AA;
                                                                                         79
235
56
179
63
25816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (lymphotoxin)
                   13.7%;
23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the gene encoding rabbit tumor
                                                                                                          Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE TUMOR NECROSIS FACTOR FAMILY.
    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rabbit TNF locus,
xin) and TNF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Azizov M.M., Jongeneel C.V.,
                                                                                                                                           TUMOR NECROSIS FACTOR.
SIGNAL-ANCHOR (TYPE-II
BY SIMILARITY.
                     Score 136.5; DB 1
Pred. No. 6.7e-05;
                                                                                                                              MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SI
                                                                                                        ISSING (IN REF. 3).
610177D0BD2EF871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       II MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakamoto H., Kajihara
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIETY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawahara
                                       DB 1;
    81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       containing the (tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISEASES, INCLUDING BY GENERAL ILL HEALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli
                                         Length
    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALSO
                                                                                                                                                                   MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL
                                           235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXISTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kiyota T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration -
    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
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01-AUG-1992 (Rel. 2
01-AUG-1992 (Rel. 2
01-NOV-1997 (Rel. 3
    CARBOHYD
SEQUENCE
                                                                      SIGNAL
                                                                                                                  PRINTS; PR01234; TNECROSISECT PRINTS; PR01236; TNFBETA. PR0SITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: LYMPHOTOXIN IS A CYTOKINE PRODUCED BY LYMPHOCYTES F
IS CYTOTOXIC FOR A WIDE RANGE OF TUNGO CELLS IN VITRO AND IN
-i- SUBUNIT: HETEROTRIMER OF EITHER TWO BETA AND ONE ALPHA SUBUNIOR (LESS PREVALENT) TWO ALPHA AND ONE BETA SUBUNITS.
-i- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIG
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Gene 102:171-178(1991).
                                                   CHAIN
                                                                                                 Cytokine;
                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                               EMBL;
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Kuhnert P., Wuethrich C., Peterha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFB_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                              S17289; S17289.
rPro; IPR000478; -.
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                                                                                               Glycoprotein;
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204 /
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23, Last sequence update)
35, Last annotation update)
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    95
21960 MW;
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                                                                                               Cytotoxin;
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N-LINKED (GLCNAC.
; 81263187435E56AC
                             LYMPHOTOXIN-ALPHA. N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
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                                                                                          Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204
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(See http://www.isb-sib.
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  . .) (POTENTIAL)
CRC64;
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Query Match
Best Local Similarity
Matches 46; Conser

Conservative

13.5%;

Score Pred.

Mismatches 134.5; No. 8.3

3.3e-05; 76;

Length

204;

33;

Gaps

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RESULT 12
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            HSSP;
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Mammalia; Eutheria;
NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT 1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (
                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-DUNKIN-HARTLEY;
MEDLINE-97462215; PubMed-9316485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P51435;
01-OCT-1996
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                             "Airway
                                                                                                                                                                                                                                                                                                                                                                                                                                          White A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yuan H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-HARTLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               factor-alpha.
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                                                                                                                                                                                              SUBUNIT: HOMOTRIMER (BY SIMILARIA).
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE
PROTEOLYTIC PROCESSING (BY SIMILARITY).
DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEA
CANCER AND INFECTION, AND IS CHARACTERIZED BY GI
                                                                                                                                                                                                                                                                                                                           FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKIN MITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
                                                                                                                                                                                                                                                                                                                 CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR TNFA
                                                                                                        European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                            SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                   CONDITIONS
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                        U39839;
U77036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----HGFL----LSNNSLLVPTSGLYFVYSQVVFSGEGCFPKATPTPLYLAHEVQLF
                                                                                                                                                                                                                                                                                                                                                                                                Physiol.
                                                                                                                                                                                                                                                                                                                                                                                                                           .M., Yoshimura T., Smith A.W., Westwi
inflammation induced by recombinant
                                                                                                                                                                                          MALNUTRITION
                                                                                                                                                                                                                                                                                                                 PROLIFERATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOV-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                       Yoshimura T.
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                        AAB06492.1;
AAB19210.1;
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                                                                                                                                                                                                                                                                                                                                                                                                273:L524-L530(1997).
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y F.J., Bingl
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o the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                INDUCE
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Hystricognathi; Caviidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                            TUMOR NECROSIS
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-91016861; PubMed=2216741;
Drews R.T., Coffee B.W., Prestwood A.K.,
"Gene sequence of porcine tumor necrosis
"Gene sequence of porcine tumor necrosis
"Sequence of porcine tumor necrosis"
"Arids Res. 18:5564-5564(1990).
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DISULFID
SEQUENCE
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                SEQUENCE OF 44-232 FROM N.A. MEDILINE-90034181; PubMed=2478420; Pauli U., Beutler B., Peterhans E.; "Porcine tumor necrosis factor alpha: chain reaction and determination of the Gene 81:185-191(1989).
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P23563;
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PRINTS; PR01235; TNFALPHA.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Cytotoxin; Transmembrane;
                                                                                                                                                                                         TISSUE-Macrophage;
Choi C.S., Molitor T.W., Lin G.F
"Complete nucleotide sequence of
                                                                                                                                                                                                                                                                                         "The porcine tumor necrosis comparative analysis."; Gene 102:171-178(1991).
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Mammalia; I
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TUMOR NECROSIS FACTOR
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EMBL; X54859; CAA38639.1; -.
EMBL; X57321; CAA40591.1; -.
EMBL; M29079; AAA31128.1; -.
PIR; S12606; S12606.
PIR; S17290.
PIR; S18965; S18965.
HSSP; P01375; ZTUN.
P36939;
01-JUN-1994 (Re
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TUMOR NECROSIS
TNF OR TNFA.
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PRINTS; PR01235; TNFALPHA.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS00259; TNF_2; 1.
Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor PROPEP 1 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002959; -.
Pfam; PF00229; TNF; 1.
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SUBCELLULAR LOCATION: TYPE
SUBCELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
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PTM: THE SOLUBLE FORM DERIVES
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           PRECURSOR (TNF-ALPHA) (CACHECTIN).
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BY SIMILARITY.
65B28F702D99C8BE CRC64;
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Pred. No.
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Best Local Similarity
Matches 45; Conser
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  Cytokine; PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO1234; TNECROSISFCT. PRINTS; PRO1235; TNFALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M59233; HSSP; P01375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peromyscus leucopus (family Cricetidae).";

Immunogenetics 35:351-353(1992).

-I- FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN I SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence of the tumor necrosis factor/cachectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=92218012; PubMed=1348497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peromyscus.
NCBI_TaxID=10041;
                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peromyscus leucopus (White-footed mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontina
                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00229; TNF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000478; -.
                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.
DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND MALNUTRITION.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONDITIONS.
SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE
EXTRACELLULAR SOLUBLE FORM.
                                                                                                                                                                           ISPLVRERGPQRVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSGH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                         ALLANGMDLKDNQLVIPADGLYLVYSQVLFKGQ
                               VNLLSAIKSPC-PKETPEGSELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQ
                                                           ILLMKSARNSCWSKDAEYG -----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS
                                                                                                                    SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 129
                                                                                                                                                    IGPQREEKFPNNLP--IIGSMAQTLTLRSSSQNSSDKPVAHVVANHQVDEQLEWLSRGAN 113
                                                                                                                                                                                                                                                                                                                                                                                             PS00251; TNF_1; 1.
PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                Cytotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002959; -.
   186
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36
148
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235
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25822
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                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Glycoprotein; Signal-anchor By SIMILARITY.
                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                        BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL); 235A5CFC9F9AC624 CRC64;
                                                                                                                                                                                                                            Score 129.5; DB 1
Pred. No. 0.00027;
                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           II MEMBRANE PROTEIN.
                                                                                                                                                                                                                Mismatches
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commercial
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01-AUG-1992
01-AUG-1992
30-MAY-2000
               DOMAIN
DISULFID
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"A 3-D model for the CD40 ligand predicts that it is a compact trimer similar to the tumor necrosis factors.";

Int. Immunol. 5:233-238(1993).

-1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF COSTINULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.

INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-92244364; PubMed-1374165;
Armitage R., Fanslow W., Sato T.A.,
Macduff B.M., Anderson D.M., Gimpel
Maliszewski C.R., Clark E.A., Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Farrah T., Smith C.A.;
"Emerging cytokine family.";
Nature 358:26-26(1992).
[3]
                                                                                                                                         MGD; MGI:88337; Thfoi
                                                                                                                                                                           EMBL; X65453; CAA46448.1; PIR; S21738; S21738.
                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                          the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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MEDLINE=93200072; PubMed=8095800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD40.",
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD40 LIGAND
                                                                                Cytokine;
                                                                                                                      InterPro; IPR000478; -. Pfam; PF00229; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 357:80-82(1992).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNF5_MOUSE
                                                                                            PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2;
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                                                      FRANSMEM
                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: SPECIFI
                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS
                                                                                                                                                                                                                                                                                                                                             T-LYMPHOCYTES
                                                                                 Transmembrane;
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(Rel. 23, Last sequence update)
(Rel. 39, Last annotation update)
(TMF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN
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Rodentia;
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                                                                              ; 1.
; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                        SPECIFICALLY
POTENTIAL. N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                  oprotein; Signal-anchor; 3D-structure.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                          EXTRACELLULAR (POTENTIAL)
                                          (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clifford K.N., Strockbine L., S.D., Davis-Smith T., C.A., Grabstein K.H., Cosman D.,
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VGLWLKPSIGSERILLKAANTHSSSQLCEQ--QSVHLGGVFELQAGASVFVNVT 241
                           QYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 171
                                                         ---QW-AKKGYYTMKSNLVMLENGKQLTVKREGLYYVYTQVTFCSNRE----PSSQRPFI
                                                                        KINSWESSRSGHSFLSNL-HLRNG-ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMV 117
                                                                                                               RQFEDLVKDITLNKEEKKENSFEMQRGDEDPQIAAHV-----VSEANSNAASVL--
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Pred. No. 0.00037;
15; Mismatches 68;
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Copyright (c) 1993 - 2000 Comp
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US-08-670-354-6
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US-08-984-842-7
US-08-996-139-13
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US-08-649-100-9
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61,	23,	Sequence 23, Appl	23,	23,	6	2,		2	Sequence 2, Appli		Sequence 11, Appl	Sequence 2, Appli	Patent No. 5180811	Patent No. 5180811	Sequence 3, Appli	Sequence 2, Appli	Sequence 1, Appli

ALIGNMENTS

RESULT 1 US-08-670-354-2

Sequence 2, Application US/08670354 Patent No. 5763223 GENERAL INFORMATION:

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-670-354-2
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-UW-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-UW-1995
FILING DATE: 29-UW-1995
                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
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TITLE OF INVENTION: Cytokine That Induces Apoptosis NUMBER OF SEQUENCES: 9
                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                      LENGTH: 281 amino acids
TYPE: amino acid
                                                                                                                                          TELEFAX: (200
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STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Kathryn A. Anderson, STREET: 51 University Street
                                                                                                                                                                  (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                           linear
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32,172
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CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-1
                                                                                                                                                                              RESULT 3
US-08-780-496-1
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                                                                                                                          Sequence 1, Application US/08780496 Patent No. 6046048 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22USO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08584031A Patent No. 6030945
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 191;
                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                       APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
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                    STREET:
                                     ADDRESSEE:
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outh San Francisco
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Pred. No. 3.8e-98;
Pred. No. 3.8e-98;
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Matches
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                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: MEMBER OF THE THE FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADBORESSE: ADBORESSEE: ADBORESSEE: 100 Abbott Park Road
STREET: 100 Abbott Park Road
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION: NAME: MATSCHARG, Diane L. REGISTRATION NUMBER: 35,66
                OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEPHAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271
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                                                                                                                                                             COUNTRY:
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                                                                                     IBM Compatible
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                    US/08/883,086
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ATTORNEY/AGENT INFORMATION:

6134.US.01

CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

DATE:

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; MOLECULE TYPE: No. 6171787e
US-08-883-086-10
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                                                                                                                                              COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 EASFFGAFLVG 281
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                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                        STREET: 51 Un:
CITY: Seattle
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STRANDEDNESS: single
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                                                                          APPLICATION NUMBER: FILING DATE: 29-JU
                                                                                                                                 CLASSIFICATION:
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                                                                          29-JUN-1995
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                                                                                            US 08/496,632
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 Mismatches

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RESULT: 6
US-09-105-343A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 996; DB 5; Best Local Similarity 100.0%; Pred. No. 3.8e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatibl
OPERATING SYSTEM: Windo
                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/U:
APPLICATION: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
ANAMY. TECKYON CASCALLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MEMBER OF THE TITLE OF INVENTION: FOR TREATMENT NUMBER OF SEQUENCES: 12
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE,DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Abbott Laboratories
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271
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                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 60064-6050
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TELEX: 75682
                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                STREET: 100 Abbot
CITY: Abbott Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 281 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INSWESSRSGHSFLSNIHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYI 120
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                                                                                                                                                                                                                    FastSEQ for Windows Version 2.0b
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                                                                                                                                                                               US/09/105,343A
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              TELEFAX: (206) 233-064
TELEX: 756822
INFORMATION FOR SEQ ID NO:
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SEQUENCE CHARACTERISTICS:
                                                               NAME: Anderson Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                           COMPOTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Vers
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
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TOPOLOGY: lin
MOLECULE TYPE:
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LENGTH: 177 amino acids
                                                                                                                                                                                                                                CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135
                                                                                                                                                                              APPLICATION NUMBER: US 08/548,368 FILING DATE: 01-NOV-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/496,632 FILING DATE: 29-JUN-1995
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 25-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
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                                                  (206) 233-0644
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                                                                                                                                                                                                                                                                                                                                         25-JUN-1996
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Pred. No. 2.1e-91;
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; TOPOLOGY: 1i; MOLECULE TYPE: PCT-US96-10895-6
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Best Local Similarity
Matches 134; Conserv
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                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 291 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: MICROSOft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
CLASSIFICATION:
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                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,17
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NUMBER OF SEQUENCES:
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APPLICATION NUMBER:
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TELEX: 756822
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                                                                                                                                                                                                                                                      FILING DATE: 0 CLASSIFICATION:
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                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
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                                                 amino acid
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51 University Street
                                                                 291 amino acids
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VENTION: Cytokine That Induces Apoptosis
                                                                                                                                  (206) 587-0430
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                                    linear
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               protein
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                                                                                                                                                                                                                                                                                       US 08/548,368
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                                                                                            US-09-105-343A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09105343A Patent No. 6207642
GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
   Best Local Similarity Matches 125; Conserv
                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US98/02859

FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:

NAME: BECKER, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6048.US.P2
                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60064-6050
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
TELEFAX: 847-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Windows Version SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MEMBER OF THE TITLE OF INVENTION: FOR TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 DMDHEASFFGAFLV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 DLDQEASFFGAFLI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 VQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 SWESSRKGHSFLNHVLFRNGELVIEQEGLYYIYSQTYFRFQEAEDASKMVSKDKVRTKQL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/105,343A FILING DATE: 12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                               TOPOLOGY:
                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKIN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQYIYKYTSYPDPIVLMKSARNSCWSRDAEYGLYSIYQGGLFELKKNDRIFVSVTNEHLM 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEE-----IKENTKNDKQM 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRTFQDTISTVPEKQLSTPPLPRGGRPQKVAAHITGITRRSNSALIPISKDGKTLGQKIE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134;
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                                                                                                                                                               amino acid
                                                                                                               TYPE:
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                                                                                                                                                                               183 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 Abbott Park Road
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abbott Laboratories
                                                                                                             No. 6207642e
                                                                                                                                               single
65.7%; Score 654; DB 4; 68.7%; Pred. No. 4.9e-62; ative 22; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.6%; Score 693; DB 5; 69.1%; Pred. No. 6.8e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                               6048.US.P2
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                                     Length 183;
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   Indels
   6;
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 Gaps
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Matches

65;

Conservative

37;

Mismatches

67;

Indels

53;

Gaps

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; MOLECULE TYPE: protein US-08-996-139-11
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US-08-996-139-11
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  Query Match
Best Local Similarity
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                                                                                                                                                                            TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION UMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: USSN 60
FILING DATE: 14 OCTOBER 199
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 00
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-KappaB
                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22 DECEMENT OF STREET PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 II 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 LV 190
                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NHVLFRNGELVIEQEGLYYIYSQTYFRFQEAEDASKMVSKDKVRTKQLVQYIYKYTSYPD 120
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                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                 NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WA
                                                                                                                                                            294 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: USSN 60/064,671
14 OCTOBER 1997
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  23.6%;
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Score 235.5; DB 3; Pred. No. 3.1e-17;
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                  Length 294;
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Query Match
Best Local Similarity 29.3
65; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11,
                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh.
OPERATING SYSTEM: Apple Operating
SOFTWARE: Microsoft Word for Power
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                     MOLECULE TYPE:
                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acid
                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: WA
                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: USSN 08/813,509 FILING DATE: 07 MARCH 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 22 DEC
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                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKISNWTLSNGKLRVNQD 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 University Street
                                                                                                                                          294 amino acids
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                                                                                                                                                                                      (206)233-0644
                                                                                                                  linear
                                                                                                                                                                                                   (206)587-0430
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14 OCTOBER 1997
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22 DECEMBER 1997
                         23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apple Operating System 7.5.5 ft Word for Power Macintosh 6.0.1
             37;
            Score 235.5;
Pred. No. 3.1e
37; Mismatches
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                           .1e-17;
                                        DB 4;
                                        Length 294;
             Indels
             53;
          Gaps
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                                                                                                                                                                                                                                                                                                                                            LENGTH: 3
TYPE: ami
TOPOLOGY:
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US-08-842-842-7; Sequence 7, Application US/08842842; Patent No. 5843678
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Relection CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OFTEN DATE:
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                161 AQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKISNMTLSNGKLRVNQD 210
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                                             149 LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Thousand Oaks
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GFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFH
                                                                                                                                        GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG 148
                                                                                                                                                                                                                                                                             SEDTLPDSCRRMKQAFQGAVQKELQHIV-----GPQRFSGAPAMMEGSWLDVAQRGKPE
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Dirk M

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RESULT 14
US-08-996-139-13
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MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
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                                                                                                          271 FYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                           211 GFYYLYANICFRHHETSGSVPTDYLQLMYYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFH 270
                                                                                                                                                                                                                                                                                                          107 SEDTLPDSCRRMKQAFQGAVQKELQHIV-----GPQRFSGAPAMMEGSWLDVAQRGKPE 160
                                                                                                                                          149 LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 190
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                                                                                                                                                                                                                                                                         34 ----AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK 89
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34.
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94304-1104
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                                                                                                                                                                                                            GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG 148
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901 California Avenue
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TD NO: 2:
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13-DEC-1996
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Pred. No. 3.5e-17;
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RESULT 15
US-08-995-659-13
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                                                                                                        Sequence 13, Appl
Patent No. 624221
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Best Local Similarity
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                                                                                         GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: USSN 00
FILING DATE: 07 MARCH 1997
             APPLICANT: Anderson, Dirk M.
APPLICANT: Gallbert, Laurent
APPLICANT: Marraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-KappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: .34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN FILING DATE: 23 DECEMBER ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
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 NUMBER OF SEQUENCES:
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STREET: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operati
                                                                                                                                                                                                                                                                                                                            94 IYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSI 152
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                                                                                                                                                                                                            NVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
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RATION NUMBER: .34,693
                                                                                                                         Application US/08995659
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Microsoft Word for Power Macintos
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Galibert,
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Ligand
19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
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Search completed: October 1, 2001, 11:43:33 Job time: 109 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION UNMBER: USSN 08/772,330

PILING DATE: 23 DECEMBER 1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
REGISTRATION UNMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430

TELEFAX: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOTECULE TYPE: STOCKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 98101
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION: CLASSIFICATION: CRESSIFICATION CONTROLLED TO THE COUNTRY CONTROLLED TO THE CONTROLLED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 23.3%; Score 232.5; DB 4; Length 317; Best Local Similarity 32.9%; Pred. No. 7.2e-17; Matches 52; Conservative 33; Mismatches 62; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
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ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                     216 LYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSI 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 IYSQTYFRFQEEIKENTKNDKQMYQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 51 Uni
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Title:
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Maximum DB seq length:
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                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                         Score
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Gapop 10.0 ,
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996
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen
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                                                                                                                                                                                                                                           Length
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2001, 11:40:13;
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                AAW76332
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                                                                                                                                                                                                                                                                                                      SUMMARIES
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555.623 Million cell updates/sec
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                                                    Tumour necrosis fa
Human Apoptosis in
Human Apoptosis in
Human apoptosis in
Novel cytokine Apo
Human TRAIL potein.
Human AGP-1. Homo
                                                                                                                                                                                                                                         Description
                  Human Apo-2 ligand 
Protein associated
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RANKL.	6724	22	152	•	32.	5
acid	8441	21	316		35.	44
	844	21	316	•	35.	43
$^{\circ}$	9102	21	316	•	35.	42
Murine TRANCE. Mu	AAY17874	20	316		35.	41
Amino acid sec	5	19	316	•		40
ŏ	301	19	316	•	35.	39
Human osteoproteg	319	19	316	•	35.	38
NF-kB receptor	829	19	294	•	35.	37
ceptoi	995	19	294		35.	36
CI	301	19	244	•	35.	ω 5
d se	27	21	172	•	ω	34
بــر	869	21	426	•	٠	ω ω
;P-1 (9	869	21	448		8	32
AGP-1.	435	19	291	•	9	31
Murine TRAIL polyp	76	19	291	•	9	30
Mouse apoptosi	978	18	291	•	9	29
Polypeptide of the	151	20	139	•	2	28
<u>a</u> 1	198	22	161	•	S	27
Q,	327	21	166	•	7	26
AGP-1	369	21	423			25
actor	363	21	220	•	53.	24
ż	701	20	281	•	7	23
AGP-1	2869	21	441		7	22
Apo-2	2701	20	281		æ	21
Apo-2	2701	20	281		æ	20
Apo-2	2701	.20	281	•	8	19
e.	151	20	281	٠	8	18
PRO10	5097	22	281	•	9	17
Apo2 1	6724	22	281	•	9	16
TL2 pol	4835	22	281	•	9	15
Apo-2	8195	21	281	•	9	14
o acid s	280	21	281	100.0	996	13
Human PRO1096	AAB24038	21	281	•	9	12

ALIGNMENTS

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RESULT
AAW76332
TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation; arthritis; septicaemia; transplant rejection; autoimmune disease inflammatory bowel disease; graft versus host disease; infection stroke; ischaemia; acute respiratory disease syndrome; psoriasis restenosis; brain injury; AIDS; bone disease; cancer; atherosclerosis; Alzheimer's disease; human; therapy; diagnosis;
                                                                 28-JUL-1997;
05-FEB-1997;
WPI; 1998-497862/43.
                    Lyn SDP, Tan KB,
                                                                                                  04-FEB-1998;
                                                                                                                                               EP867509-A2.
                                                                                                                                                                                                                                                                                 Human TL2 (TRAIL), ligand for TR5.
                                                                                                                                                                                                                                                                                                     11-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                               AAW76332;
                                                                                                                                                                                                                                                                                                                                                     AAW76332 standard; Protein;
                                         (SMIK)
                                                                                                                        30-SEP-1998.
                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                         ligand.
                                          SMITHKLINE BEECHAM CORP.
                                                                  97US-0901469.
97US-0795910.
                                                                                                  98EP-0300827
                    Truneh A,
                                                                                                                                                                                                                                                                                                                                                     279
                     Young PR;
                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                    ne disease;
infection;
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AAW95032
ID AAW9
XX AAW9
AC AAW9
AC AAW9
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XX TUMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of human TL2 (also known as TRAIL), which has newly been discovered to be a ligand of human tumour necrosis related receptor TR5 (see AAW76331). This TR5 polypeptide of the invention and TL2 can be used in screening processes for compounds which bind the receptor, or its ligand, and which activate (agonists) or inhibit (antagonists) the receptor or TL2. Treatment of a subject with the need to inhibit TR5 polypeptide activity comprises administering an antagonist to the polypeptide, administering a nucleic acid that inhibits the expression of the nucleotide sequence encoding the polypeptide and/or administering a polypeptide that competes with the polypeptide for its ligand, substrate or receptor. The active agents can be used for the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atheroscelerosis and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis,
                                                                                          EP897114-A2
                                                                                                                                                                                                                athersclerosis;
                                                                                                                                                                                                                                                                    inflammation; septicemia; autoimmune disease; transplant rejection;
graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                  Tumour necrosis factor receptor; TNF-R;
                                                                                                                                                                                                                                                                                                                                                                                       Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                               acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW95032 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
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                                                                                                                                                                                                                                     respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279
                                                                                                                                                                                                                                           disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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's disease.
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Pred. No. 3.4e-94;
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                                                                                                                                                                                                                                                                                                                                  TR1; TR2; TL2; TL4; arthritis;
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RESULT
AAW27134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to identifying agonists or antagonists to tumour concerns factor receptor (TNP-R) related polypeptides (TR1 and TR2, TL2 and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a candidate compound in the presence of TL2 or TL4; or (11) contacting TL2 or TL4 with a candidate compound in the presence of TR1 or TR2; and (b) assessing the ability of the candidate compound to compete with TR1 or TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful for treating diseases caused by imbalance of TL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, transplant rejection, graft vs. host disease, infection, stroke, ischemia, acute respiratory disease syndrome, concerns the transplant rejection of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 191; Conserv
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13-AUG-1997;
26-AUG-1997;
                                                                 Apoptosis inducing molecule-I; AIM-I; autoimmune disorder; tumour necrosis factor ligand superfamily; AIM-I altered expression; neoplasia inhibition; anti-inflammatory agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying agonists and antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) useful for treating stroke, Alzheimer's disease and AIDS
                                                                                                                                                                                                                        02-APR-1998
                                                                                                                                                                                                                                                                                                                           AAW27134 standard; Protein; 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 14-15; 18pp; English.
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97US-0055513.
97US-0056980.
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                                                                                                                                                                    molecule-I
                                                                                                                                                                      (AIM-I).
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Best Local S
Matches 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a human Apoptosis inducing molecule-I (AIM-I). AIM-I is a member of the tumour necrosis factor (TNR) ligand superfamily. The products can be used in the diagnosis and treatment disorders related to under-expression, over-expression or altered expression of AIM-I. AIM. I or agonists can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated apoptosis inducing molecule-I - used to develop products for the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft versus host disease or inflammation.
Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
                           Human apoptosis inducer cytokine TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-inflammatory agents, for treating endotoxic shock or to prevent {\tt activation} of {\tt HIV}.
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N-PSDB; AAT85210.
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                                                                                                                 AAW19787 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                          24-SEP-1997
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191; Conserv
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Pred. No. 3.4e-94;
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Matches 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRAIL, a novel cytokine, induces apoptosis in cancer a virus-infected cells - useful for treating thrombotic microangiopathy, cancer and viral infection and for useful control in the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Domain
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29-JUN-1995;
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EASFFGAFLVG
                                               ykytsypdpillmksarnscwskdaeyglysiyqggifelkendrifvsvtnehlidmdh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
                                                                                                                                                                                                                                                                                                                                    100.0%; llarity 100.0%; Conservative 0;
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95US-0496632.
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89..90
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39..281
/label= Extracelular_domain
/note= "contains a receptor-binding region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=_"potential KEX2 protease processing site"
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Pred. No. 3.4e-94;
; Mismatches 0;
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AAW19777
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A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian cell apoptosis. It is belived to be a member of the tumour necrosis factor cytokine family. Its amino acid sequence was deduced from a cDNA clone (AAT72796) isolated from a human placental cDNA library. Apo-2 ligand polypeptides, esp. those corresponding to amino acids 114-281, 14-281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells transformed or transfected with a vector contg. Apo-2 ligand nucleic acid. They can be used to induce apoptosis in mammals and to treat pathological conditions such as cancer (esp. breast or colon cancer) or to raise antibodies useful in diagnostic assays.
Sequence
                                                                                                                                                            Claim 4; Fig la; 72pp; English.
                                                                                                                                                                                   Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce apoptosis for the treatment of breast and colon cancer
                                                                                                                                                                                                                    N-PSDB; AAT72796
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                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
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41..28
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109
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                                                                                                                                                                                                                                                                                                                                                                                                           /label= Glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Cytoplasmic_region
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       This sequence represents the human tumour necrosis factor (TNF)-relative receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRAIL). This protein is used in a method resulting in the isolation of the novel human TNF related receptor, TR6 polypeptides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, infection, stroke, ischaemia, acut respiratory disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transplant rejection; infection; ischaemia; brain injury; bone disease; acute respiratory disease syndrome; acquired autoimmune disease syndrome; AIDS; cancer; atherosclerosis; Alzhelmers disease; TRAIL; TNF; TL2.
                                                                                                                                                                                           Disclosure; Page 32-33;
                                                                                                                                                                                                                       DNA encoding tumour necrosis factor receptor TR6 - polypeptide, antibody, agonist, antagonist, etc
                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                          09-MAY-1997;
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14-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour necrosis
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97US-0041230.
97US-0853684.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor-related apoptosis-inducing ligand
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Mismatches
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hes 0;
              and Alzheimers disease
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                                                                                                                                                               (TNF)-related
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Best Local
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29-JUN-1995;
01-NOV-1995;
apoptosis of Jurkat cells.
          This represents a human tumour (TRAIL) polypeptide. The human
                                                       DNA encoding cytokine TNF-related apoptosis ligand polypeptides useful for producing recombinant polypeptides for research and therapy of leukaemia, lymphoma, melanoma and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW56760 standard; Protein; 281 AA
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                                                                                                                                                                                                    25-JUN-1996;
                                                                                                                                                                                                                     09-JUN-1998
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                                                                                                                                                                                                                                                                     Domain
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                                                                                                                                                                                                                                                                                                                                                       cytokine;
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                                                                                                       1998-347322/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYI 120
                                                                                                                                                                                                                                                                                                                                                                                  TRAIL
                                                                                                                                                                                                                                                                                                                                                               necrosis factor related apoptosis ligand; TRAIL; research; human;
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                                      Columns
                                                                                                                                                                                                                                                                                                                                                      therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                        Wiley SR
                                                                                                                                                            96US-0670354.
95US-0496632.
95US-0548368.
                                                                                                                                                                                                   96US-0670354
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1..18
                                                                                                                                                                                                                                                                    /note=
39..28]
                                                                                                                                                                                                                                                                                      /note=
19..38
                                      33-36;
                                                                                                                                                                                                                                                                                                                                                      leukaemia; lymphoma; melanoma; viral infection
The human cells. The
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                                                                                                                                                                                                                                                                            "transmembrane region"
                                                                                                                                                                                                                                                                                              "N-terminal cytoplasmic domain"
                                                                                                                                                                                                                                                         "extracellular domain"
                                    28pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 3.4e-94;
                                     English.
necrosis factor related apoptosis ligand
and murine TRAIL polypeptides can induce
encoding nucleic acid sequences are usefi
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Best Local
The present sequence represents human AGP-1. AGP-1 is a tumour-necrosifactor (TNF)-related protein, involved in inflammation, myelopoiesis and bone resorption. It has the same nucleic acid and amino acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRAIL) describe in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay reagents for detecting AGP-1 expression. Nucleic acid complementary to AGP-1 is used to regulate AGP-1 expression and antagonistic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells (e.g. to isolate antigens for vaccine development). The polypeptides ce used to treat leukaemia, lymphoma or melanoma (e.g. by extracorpore treatment of blood or bone-marrow), or to treat viral infections.
                                                                                                                                                                WPI; 1998-042194/04
N-PSDB; AAV15295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW44354;
                                                                                             Claim 7; Page 36-37;
                                                                                                                    haematopoietic
                                                                                                                            Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein useful for treating inflammation, bone resorption a
                                                                                                                                                                                                    Danilenko
                                                                                                                                                                                                                                                 07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   inflammation;
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                                                                                                                                                                                                                          (AMGE-) AMGEN
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                                                                                                                                                                                                                                                                                                                                                                   bone
                                                                                                                                                                                                                                                                                                                                                                 tumour necrosis factor-related protein; TNF; bone resorption; haematopoletic disease.
                                                                                                                    diseases
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                                                                                                                              inflammation, bone resorption and
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                                                                     AGP-1 is a tumour-necrosis
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Best Local S
Matches 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus erythematosus, psoriasis, scleroderma, infection-related inflammation) or bone resorption diseases (e.g. osteopporosis, osteomyelitis, hypercalcaemia, Paget's disease). AGP-1 can be used to treat haematopoietic diseases associated with reduction in the number of bone marrow cells, particularly neutrophils and lymphocytes, e.g. where caused by disease, injury or exposure to myelosuppressive agents. Host cells, transformed with expression vectors containing AGP-1 DNA, are used to produce recombinant AGP-1.
            This
 This sequence (Apo-2L). The
                                Claim 1; Fig 1A; 86pp; English.
                                                     A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis in mammalian cancer cells
                                                                                                                                                                                                                                                    W09936535-A1
                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                         Cytokine;
                                                                                                                                                                                                                                                                                                                           Human Apo-2 ligand (Apo-2L)
                                                                                                                                                                                                                                                                                                                                                   24-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                       AAY27012;
                                                                                                                                                                                                                                                                                                                                                                                            AAY27012 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                 Ashkenazi AJ,
                                                                                                                                                                           15-APR-1998;
15-JAN-1998;
                                                                                                                                                                                                                               22-JUL-1999
                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                           15-JAN-1999;
                                                                                                                                                                                                                                                                                           Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune lupus; immune-mediated glomerular nephritis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                      1999-444397/37.
DB; AAX86987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 AA;
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                                                                                                                                                                                                                                                                                                                                                 (first
represents a novel Apo-2L polypeptide
                                                                                                                                                                          98US-0060533
98US-0007886
                                                                                                                                Kelley
                                                                                                                                                                                                           99WO-US01039
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                                                                                                                                 RF,
                                                                                                                                                                                                                                                                                                                             polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 996; DB 19;
Pred: No. 3.4e-94;
; Mismatches 0;
                                                                                                                                 MT,
cytokine,
e produced
                                                                                                                                  Pitti
designated l by standard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                        disorder;
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human c

Apo-2

The specification describes the use a polypeptide corresponding to at least the primary sequence of part of the present sequence to produce a diagnostic, prophylactic or therapeutic composition useful in cases

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RESULT 1
AAY01517
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Best Local S
Matches 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immune-mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-2L antibodies can be used for treating diseases
                                                                        Use of polypeptide derived from TRAIL protein for diagnosis of degenerative disease - autoimmunity and inflammation, also use prevention or treatment, and similar use of corresponding ligation nucleic acid
                                                                                                                                                                                                                                                                                                                                          surface receptor;
                                                 Claim
                                                                                                                                        WPI; 1999-156177/14.
                                                                                                                                                                Belliveau JF,
                                                                                                                                                                                                                 04-AUG-1997;
                                                                                                                                                                                                                                         04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                       Neurodegenerative disease; autoimmune disease; lupus erythematosus; rhuematoid arthritis; SEP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY01517 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                           FR2766713-A1
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            Protein associated with neurodegenerative and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAY-1999
                                                                                                                                                                                      (INMR ) BIO MERIEUX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFYSVTNEHLIDMDH 180
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                                                                                                                                                                                                                                                                                                                                       erythematosus; rhuematoru erythematoru receptor; TRAIL protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     easffgaflvg
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                                                 13;
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                                             21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
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                                                 French.
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Pred. No. 3.4e-94;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                        apoptotic;
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                                                                                    o useful
| ligand a
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Best Local S
Matches 191
                                  Fusion protein of AGP-1 protein proliferative disorders, immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a marker of disease and a therapeutic target, e.g. its apoptotic activity can be blocked with an anti-TRAIL antibody or a TRAIL equivalent that binds to specific receptors, inhibiting formation of natural complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of degenerative, autoimmune and inflammatory diseases. The polypeptide can be used in treatment of neurodegenerative disease, lupus erythematosus, rhuematoid arthritis, and SEP. The polypeptides are apoptotic in central nervous system cells, antigenic and specifically recognise the surface receptor of the TRAIL protein. The polypeptide
             Claim
                                                                                                                                                                                                                                                                                                   antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; l
human immunodeficiency virus; apoptosis; proliferative disorder;
cancer; hepatitis; acquired immunodeficiency syndrome; AIDS;
autoimmune disorder; transplant rejection; cardiovascular diseas;
                                                                                                                                                                                                                                           WO200063253-A1.
                                                                                                                                                                                                                                                                                         arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                           Human AGP-1.
                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2001
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                                                                                    N-PSDB;
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                                                                                                                                            (AMGE-)
                                                                                                                                                                    16-APR-1999;
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| easffgaflvg
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                                                                                   2000-665240/64.
DB; AAC67831.
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             ω
                                                                                                                                                                                                                                                                                                                                                  AGP-1; type II transmembrane protein; cytostatic; antiviral;
                                                                                                                     Meng
           Fig
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            93pp;
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             English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 996; DB 20;
Pred. No. 3.4e-94;
                                               and an Fc region, used to trea disorders, and virally-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                      disease;
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RESULT 12
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Best Local :
                                                                                                                        08-MAR-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human AGP-1, a type II transmembrane protein. Fusion proteins comprising an FC immunoglobulin region fused to the N-terminal portion of the AGP-1 protein have been produced. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins have increased biological activity compared to the soluble AGP-1 proteins used in prior art therapies.
Antibodies the growth
                                                                                                                                                                                                                                                                                                          Human PRO1096 protein sequence SEQ
                                   N-PSDB;
                                                                 Botstein D,
                                                                                                                                                                                 02-DEC-1999;
                                                                                                                                                                                                                             WO200053750-A1
                                                                                                                                                                                                                                                                                                                                 25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                       AAB24038;
                                                                                                                                                                                                                                                                                                                                                                             AAB24038 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                         identification;
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s specific f
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                                                                   Goddard
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                                                                                                                        99WO-US20111.
99US-0162506.
99WO-US28313.
                                                                                                                                                                                                                                                                                   diagnosis;
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                                                                                                              99WO-US28634
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PRO polypeptides, used to diagnose and mammals, and to identify inhibitors of
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                                                                   Gurney
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Pred. No. 3.4e-94;
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                                                                                                                                                                                                                                                                         anticancer;
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                                                                 Roy
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                                                                   MA,
                                                                                                                                                                                                                                                                         e; proliferation; detection.
                                                                    Watanabe
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PRO
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XX AABO
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XX AMIN
DE AMIN
XX Huma
KW TRAI
KW TRAI
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XX HOMO
OS HOMO
XX WO2C
XX IS-F
PN 24-A
PF 15-F
XX IS-F
PR 16-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an antibody that binds to a human CC protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; CC PRO3434; PRO1927; PRO1557; PRO1293; PRO1303; PRO4334; PRO4354; PRO4397; PRO1927; PRO1555; PRO1293; PRO1303; PRO4362. (I) has contacted with test calls: Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), contacted with test calls: Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), contacted which contacted which contacted which contacted which inhibit the activity of (I), contacted which inhibit the biological activity contacted contacted to AAC58102 represent form the present invention probes used in examples from the present invention for human PRO sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human protein sequences given in the exemplification of the propersent contacted and protein sequences given in the exemplification of the contacted and protein sequences given in the exemplification of the contacted and protein sequences given in the exemplification of the contacted and protein sequences given in the exemplification of the contacted and protein sequences given in the exemplification of the contacted and protein sequences given in the exemplification of the contacted and protein sequences given in the exemplification of the contacted and protein sequences given in the exemplification of the contacted and protein sequences given in the exemplification of the contacted and protein sequences given in the exemplification of the contacted and protein sequences given in the present invention for the contacted and protein sequences given in the present invention for the contacted and protein seque
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Best Local Similarity
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                        (STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                   24 - AUG - 2000
                                                                                                                                                                                                                  WO200048619-A1
                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                 non-small cell
                                                                                                                                                                                                                                                                                                                                  TNF related apoptosis-inducing ligand; tumour corrall receptor ligand; solid tumour; carcinoma;
                                                                                                                                                                                                                                                                                                                                                        Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide; TNF related apoptosis-inducing ligand; tumour cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a human TRAIL polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB08545 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                       16-FEB-1999;
                                                                                                                    15-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide and protein sequences given in the exemplification present invention.
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                                                                                                                       2000WO-US03891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                              lung carcinoma.
                                                                       99US-0120313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
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Best Local Similarity 100.0%;
Matches 191; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a human TRAIL (tumour necrosis factor (TNF) related apoptosis-inducing ligand) polypeptide. The specification describes a method for enhanced killing of tumour cells. The method comprises contacting a susceptible tumour cell with a synergistic mixture of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined dosage to kill at least 50 % of the cells. This mixture is synergistic, and so is active at lower doses and against otherwise resistant cell lines. The method is used for killing tumour cells, especially solid tumours or carcinomas (especially mammary carcinoma or non-small cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Killing of tumour cells, e.g. solid tumours or carcinoma, administration of synergistic combination of diterpenoid cumour necrosis factor related apoptosis-inducing ligand.
                         Kim KJ,
                                                                                                                                               09-JAN-1996;
                                                                                                                                                                                                         08-JAN-1997;
                                                                                                                                                                                                                                                                        04-APR-2000
                                                                                                                                                                                                                                                                                                                                     US6046048-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo-2 ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Apo-2 ligand protein sequence
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N-PSDB; AAA64325.
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; apoptosis; cancer
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                                                                                  (GETH ) GENENTECH INC.
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                         Ashkenazi AJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human;
                                                                                                                                               96US-0009755
                                                                                                                                                                                                         97US-0780496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody; hybridoma cell line; diagnosis;
                         Chuntharapai A;
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Pred. No. 3.4e-94;
0; Mismatches 0;
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RESULT JAAB48350 ID AAB48350 AAC AABA XX AABA XX TUME MW ANTL KW ANTL 
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Best Local
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                                                                                                                                                                                                                                                                                                                           Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2; antiinflammatory; immunosuppressive; cerebroprotective; vasotropic; antiastbmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic; nootropic; neuroprotective; antiarthritic; antirheumatic; antiischemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig la; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated monoclonal antibodies having antigen specificity for Apo-2 ligand, e.g. 266, 2Ell or 5C2, useful for detecting the expression of Apo-2 ligand serum, and for treating diseases associated with increased apoptosis
                                  12-JUN-2000; 2000WO-US16134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human TL2 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB48350 standard; Protein; 281
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                                                                                                   21-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                        therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a human tumour necrosis factor (TNF) related receptor, TR6. TR6 can be expressed by standard recombinant methodology. The TR6 polypeptides are useful for treating chronic and acute inflammation, rheumatoid arthritis, septicemia, autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tumor necrosis factor related receptor TR6 polynucleotides and polypeptides useful for e.g. for treating chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, infection cancer, bone diseases
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SUMMARIES

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144 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 188 : : : : :: :: : : 166 DAEYALHSVYQGGLFELRAGDEVFVSVSSPTMVYGEDSSSYFGAF 210	85 VIHEKGFYYIYSQTYFRF-QEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 143 :: : : 106 RVPQDGRYYLYSQVYFRYPSPSDSDQSSVSHQLVQCIYKKTSYLNPIQLLKGVGTKCWAP 165	30 QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGEL 84 : : :	Query Match 30.7%; Score 305.5; DB 13; Length 214; Best Local Similarity 37.6%; Pred. No. 1.2e-19; Matches 62; Conservative 37; Mismatches 59; Indels 7; Gaps	EMBL; AF250041; AAG47640.1; SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;	Comp. Biochem. Physiol. 0:0-0(2001).	"Molecular cloudy and expression of a TNF receptor and two TNF	SEQUENCE FROM N.A. HODE J. GOETZ F.W.:	I_TaxID=7955;	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.	<pre>Brachydanio rerio (debratish) (debra danio). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</pre>	TRAIL-LIKE PROTEIN.	16, 16,	(TrEMBLrel.	Z5 Q9DDZ5 PRELIMINARY; PRT; 214 AA.	1

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01-0CT-2000 (TremBLrel. 15,
01-0CT-2000 (TremBLrel. 15,
01-MAR-2001 (TremBLrel. 16,
RECEPTOR ACTIVATOR OF NF-KB
                                                        "Receptor activator of NF-kB ligand Submitted (SEP-1999) to the EMBL/GerEMBL, AB032771; BAA97257.1; -
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Mammalia; Eutheria;
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EMBL; AB022036; BAA36970.1;
EMBL; AB022037; BAA36970.1;
EMBL; AB022038; BAA36970.1;
INTEXPROS [PRO00478; -...
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Gene 230:121-127(1999).
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Mus musculus (Mouse).
PROSITE;
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"Cloning and characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246; DB 11;
No. 3.7e-14;
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Matches 62
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Q9JJK8;
Q1-OCT-2000
01-OCT-2000
01-MAR-2001
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Mus musculus (Mouse).
"-rvota; Metazoa; Chordata;
"-rvota; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003263; -.

pfam; pF00229; TNF; 1.

ProDom; pD008600; -; 1.

PROSITE; PS50049; TNF_2; 1.

SEQUENCE 199 AA; 22150 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1999) to the EMBL; AB032772; BAA97258.1; InterPro; IPR000478; -. InterPro; IPR003263; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Somatostatin, a new RANKL isoforms.";
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173
                                        168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 SEETI-----STVQEKQQNISPLVRERGPQRVA-------
                                                                                                                    NTKNDKQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSTYQGGIFELKENDRIF
                                                                                                                                                                                                                                                                                                                 VQEKQQNISPLVRERGPQRVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV
IQVSNPSLLDPDQDATYFGAFKV
                                     VSVTNEHLIDMDHEASFFGAFLV
                                                                                     VPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEIS
                                                                                                                                                                                                    PNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQPFAHLT-'---INAASIPSGSHKVTL----SSWYHDR-GWAKISNMTLSNGKLRVNQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEDTLPDSCRRMKQAFQGAVQKELQHIV-----GPQRFSGAPAMMEGSWLDVAQRGKPE
                                                                                                                                                                               PSGSHKVTL----SSWYHDR-GWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGS
                                                                                                                                                                                                                                                                         VQKELQHIV----
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                                                                                                                                                                                                                                                                                                                                                              l Similarity
62; Conser
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Pred.
195
                                        190
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Pred. No. 2.7
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nes 65;
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1.8e-13;
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Q9ESE2;
01-MAR-2001
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01-MAR-2001
                                                                                                                                                                                                                                    01-OCT-2000
01-OCT-2000
01-MAR-2001
FAS LIGAND.
                                                                               SPECIES-M.nemestrina; STRAIN-PIG-TA.
Kirii Y., Inoue T., Yoshino K.;
"Pig-talled monkey Fas ligand mRNA,
                                                                                                                                                              Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                             PT-FASL OR CM-FASL OR RM-FASL.
Macaca nemestrina (Pig-tailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, sequence and functional characterization homologue of receptor activator of NF-kB ligand."; J. Bone Miner. Res. 15:2178-2186(2000).

EMBL; AF187319; AAG17031.1; -.
SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, RECEPTOR ACTIVATOR OF NF-KB
SPECIES-M. fascicularis; STRAIN-CYNOMOLGUS MONKEY, Kiril Y., Inoue T., Yoshino K.; "Cynomolgus monkey Pas ligand mRNA, complete cds."Cynomolgus monkey Pas ligand mRNA, complete cds. Submitted (NOV-1999) to the EMBL/GenBank/DDBJ dai
                                                                                                                                         Cercopithecinae;
NCBI_TaxID-9545;
                                                                                                                                                                                                                                                                                    Q9MYL6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
PubMed=11092398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                            SEQUENCE FROM N.A.
                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                         KQMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQEKQQNISPLVRERGPQR---VAAHITGT-----RGRS------NTLSSPNSKN' 53
                                                                                                                                                                                                                                                                                                                                                          PSLLDPDQDATYFGAFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVSL---
                                                                                                                                                                                                                                                                                                                                                                                                       LQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISVQVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQRELQHIV-----GPQRFSGVPAMMEGSWLDVARRGKPEAQPFAHLTINAADIPSGSH
                                                                                                                                                                                               nemestrina (Pig-tailed macaque), fascicularis (Crab eating macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tan J., Huang
                                                                     (NOV-1999)
                                                                                                                                                                                                                                              0 (TrembLrel. 15, 0 (TrembLrel. 15, 15) (TrembLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SSWYHDR-GWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPADY
                                                                                                                                          Macaca.
9541, 9544;
                                                                                           a; STRAIN=PIG-TAILED MONKEY; Yoshino K.;
                                                                     to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ľ.,
                                                                                                                                                                                                                                                                                                                                                                                 190
                                                                                                                                                                                                                                                                                                                                                          314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gao
                                                                                                                                                                                                                                                  Created)
Last sequence
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence up
nd mRNA, complete cds.";
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                             Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Х.Н.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4B87A4D706AD098F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                  sequence u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232.5; DB 1
No. 5.9e-13;
                                                                                 complete cds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laird
                                                                                                                                                                                                                                                                                                 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318
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                                                                                                                                                                Cercopithecidae,
                                                                                                                                                                                                  (Cynomolgus monkey), and
                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0f
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; Murinae; Rat
                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rat
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N [3]

P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

SPECIES-M.mulatta; STRAIN=RHESUS MONKEY;

RI Kirii Y., Inoue T., Yoshino K.;

RT "Rhesus monkey Fas ligand mRNA, complete cds.";

RL Submitted (NOY-1999) to the EMBL/GenBank/DDBJ databases.

BR EMBL; AB035140; BAA90296.1; -.

DR EMBL; AB035138; BAA90294.1; -.

DR EMBL; AB035139; BAA90295.1; -.

DR EMBL; AB035139; BAA90295.1; -.

DR InterPro; IPR000478; -.

DR Pfam; PF00229; TNF; 1.

DR PROSITE; PS00229; TNF_1; 1.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS000251; TNF_1; 1.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS000251; TNF_1; 1.
                                                                                                                      9WV900
1D 9WV900
1D 000
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Best Local S
Matches 52
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9WV90;
01-NOV-1999
01-NOV-1999
01-MAR-2001
                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                                                       SMART; S
                                                                                                                                                                                                                                                                                                                     chronic woodchuck viral hepatitis."; Clin. Exp. Immunol. 0:0-0(1999). EMBL; AF152368; AAD38387.1; -.
                                                                                                                                                                                                                   Pfam; PF00229; TNF; 1.
PROSITE; PS00251; TNF_1;
PROSITE; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-HEALTHY LIVER;
Hodgson P.D., Grant M.D., Michalak T.
"Perforin and Fas/Fas ligand-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAS LIGAND (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9WV90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marmota.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marmota monax (Woodchuck).
                                                                                                                                                                                                                                                                                             InterPro; IPR000478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFGAF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSQKHTASSLEKQIGHPSPPPEKKEQRKVAHLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKYPQDLVMMEGKMMS-YCTTGQMWAHSSYLGAVFNLTSADHLYVNVSELSLVNFEESQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDT-YGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQ-----SCTNLPLSHKVYMRN
                                                                                                                                                                                              SM00207;
ch 17.3%; similarity 28.4%; 52; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                         169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 (TrEMBLrel. 12,
9 (TrEMBLrel. 12,
1 (TrEMBLrel. 16,
                                                                                                                                                  169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                         AΑ;
                                                                                                                                                                                              TNF;
                                                                                                                                                  169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                         19274 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Michalak T.I.;
  35;
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Pred. No. 1.3e
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation updat
Score 172; DE
Pred. No. 6.56
85; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                         FDE395B014717B6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169
                                                                                                                                                                                                                                                                                                                                                                                             cytotoxicity
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DB 11;
.5e-08;
es 56;
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.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                           Length 169;
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                               acute
  40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 095150 O9 AC 09 DT 01 DT 01 DT 01
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Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tregaskes C.A., Young J.R., Burnside J.,
"cloning of a putative chicken CD40 ligand.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ dat
EMBL; AJ243435; CAB95748.1; -.
Interpro; IPR000478; -.
pfam; pF00229; TNF; 1.
pROSITE; PS00251; TNF_1; 1.
pROSITE; PS0049; TNF_2; 1.
SEQUENCE 272 AA; 30862 MW; 5409F24A8E53CCD7 (
                                 095150;
095150;
01-MAY-1999
01-MAY-1999
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0918D8;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
PUTATIVE CD154 (CD40 LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Garronta: Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-WHITE LEGHORN LINE 0; TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQJENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0918D8
                                                                                                                                                                                                                                                257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                                                                                                                                                                                                                                                                                                                                            RTASEELPKFEMHRSHEHPHLKSRNETSVAEEKRQPIATHLAGV--KSNTTV-----
                                                                                                                                                                                                                                              AVNVNPGNTYFGMF
                                                                                                                                                                                                                                                                                         LIDMDHEASFFGAF
                                                                                                                                                                                                                                                                                                                                      PFTLYIYLYLPMEEDRLLMKGLDTHSTS-TALCELQSIREGGVFELRQGDMVFVNVTDST 256
                                                                                                                                                                                                                                                                                                                                                              QMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTSEETISTVQEKQQNISPLVRERGP-----QRVAAHITGTRGRSNTLSSPNSKNEK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DMD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSKYPQDLVLMEGKMMNYCTTGQMWAR-----SSYLGAVFNFTSNDHLYVNVSELSLI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEDT-YGISLISGVKYQKGGLVINDTGLYFYYSKIYFRGQ-----SCNNQPLSHKYYVK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNTEPSL----EKQIGHPSSPSDKKALRRAAHLT---GKPNSRSSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167
                                      (TrEMBLrel.
                                                                                 (TrEMBLrel.
                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neognathae;
                                                                                                                                                                                                                                                                                           188
                                                                                                                                                                                                                                              270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.6%;
27.3%;
                                   10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
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Last sequence update)
Last annotation update)
                                   Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 165; DB 13;
Pred. No. 4.9e-07;
2; Mismatches 77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5409F24A8E53CCD7 CRC64;
                                                                                                                              174
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                                                      update)
                                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              CTKAAASA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΈE
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                                                                                                                                                                                                                                                                                                                                                                                   174
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OPOXHE

OPOXHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO; IPRUVULLE.
INTERPRO; IPRUVULLE.
PEAM; PE00229; TNF; 1.
PRINTS; PR01234; TNECROSISECT.
PRODOM; PD002012; "; 1.
R PROSITE; PS50049; TNF_2; 1.
SMART; SM00207; TNF; 1.
SMART; COTTENCE 174 AA; 20131 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QYH9;
Q9QYH9;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                                   pathway.";
Submitted
                                                                                                                                                                                                                                                               TISSUE=FETAL LIVER CELL;
Misawa K., Nosaka T., Kitamura T., I
"Murine LIGHT, a homologue of human
                                                                                                                                               SEQUENCE FROM N.A. Tamada K., Shimoza
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000478; -. InterPro; IPR003636; -. Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-1997)
EMBL; AF039390; AADO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                    Submitted (JUN-1999)
                                                                                                                                                                                                                                              tamily
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01375; 4TSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiogenesis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VASCULAR ENDOTHELIAL CELL GROWTH INHIBITOR VEGI.
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISLVDYTKEDKTFFGAFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN (LIGAND FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 35.149; Conservative
                                   (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1997) to the AAD08783.1;
                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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TISSUE-VASCULAR ENDOTHELIAL;
Yu G.-L., Zhai Y., Ni J., Iruela-Arispe
Lu J., Kozak D., Jiang G.-W., Rojas L.,
Gentz S., Lippman M.E., Aggarwal B.B., F
                          Tamada K., Shimozaki K., Chapoval A.I., Zhu G. Ullrich S., Chen S.F., Sica G., Flies D., Hsie Nagata S., Ni J., Chen L.;
"Modulation of cell-mediated immunity through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yu G.-L.;
"A Novel-Endothelial Cell-Specific Negative Regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WESSRSGHSFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQ----EEIKENTKNDK--QM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVVITKVTDSYPEPTQLLMGTKSVC-----EVGSNWFQPIYLGAMFSLQEGDKLMVNVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG---LYSIYQGGIFELKENDRIFVSVTN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WE-HELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSI 100
                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
(IN (LIGAND FOR HERPESVIRUS ENTRY MEDIATOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 160; Pred. No. 7.8e. 24; Mismatches
                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCB83BA7EE673B98
                                                       I A.I., L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160;
                                                                                                                                                                                     Kojima
                                                                                                                                                                  Kojima T.;
LIGHT which
                                                                                                                                                                                                                                                                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben
                                                                Zhu G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L., Huang W.-Q., Xing L.,
Janat M.F., Buergin M.,
Ruben S., Gentz R., Li L.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
.8e-07;
                                                                                                                                                                                                                                                                       Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                LIGHT
databases
                                                                Su J.,
S.L., 1
                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                    a member
                                costimulatory
                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                         Murinae; Mus
                                                                 HSu
                                                                                                                                                                                                                                                                                                                                             (LIGHT).
                                                              Zhai Y.
Hsu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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                                                                                                                                                                     of
                                                                 Fu
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RESULT 11
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Best Local Similarity
Matches 47; Conserv
 Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=LYMPHOMA;
Force W.R., Todd P.K., Mikayama T.;
Force W.R., Todd P.K., Mikayama T.;
"Mouse LIGHT; Molecular Genetics, Ligand Binding and Expression.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB029155; BAA88559.1; -.
EMBL; AF123385; AAF76453.1; -.
EMBL; AF227533; AAF36722.1; -.
EMBL; AF227533; AAF36722.1; -.
HSSP; P01175; 4TSV.
                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLRel. 16, Last annotation update)
TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                      MEDLINE-98234044; PubMed-9573100; Melby P.C., Tryon V.V., Chandrasekar B., "Cloning of Syrian hamster (Mesocricetus analysis of cytokine mRNA expression in eleishmaniasis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000478; -.

Pfam; PF00229; TNF; 1.

PRINTS; PR01234; TNECROSISFCT.

PROSITE; PS50049; TNF_2; 1.

SEQUENCE 239 AA; 26338 MW;
                                                                             NON_TER
                                                                                                                 PRINTS; PR01234; TNECROSISFCT PROSITE; PS00251; TNF_1; 1. PR0SITE; PS50049; TNF_2; 1.
                                                                                                                                                                                  EMBL; AF046215; AAC40100.1; HSSP; P06804; 2TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     078332
                                                                                                       SMART; SM00207;
                                                                                                                                                         Pfam; PF00229; TNF; 1
                                                                                                                                                                                                                                                                                           TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                               Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE FROM
                                                                                                                                                                        InterPro; IPR000478; -.
                                                                                                                                                                                                            Infect. Immun. 66:2135-2142(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 SIYQGGIFELKENDRIFVSVTNEHLI-DMDHEASFFGAFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSFLGGVVHLEAGEEVVVRVPGNRLVRPRDGTRSYFGAFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS-YPDPILLMKSARNSCWSKDAEYGLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAHLTGANASLIGIGGP------LIWE-TRLGLAFLRGLTYHDGALVTMEPGYY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YVYSKVQLS-GVGCPQGLANGLPITHGLYKRTSRYPKELELLVSRRSPCGRANSSRVWWD
                                                              216
216 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.
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                                                                                                TNF;
                                                               216
23793
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            14.5%;
                                                               WW;
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  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 152.5;
Pred. No. 5.4e
25; Mismatches
            Score 144.5; DB 1
Pred. No. 2.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                BADAE3F83F45B533 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217874AC71AD6BE3 CRC64;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.4e-06;
nes 72;
                                                                                                                                                                                                                                      experimental
                                                                                                                                                                                                                                                   auratus) cytokine
                                                                                                                                                                                                                                                               Freeman G.L.;
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                          DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190
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 Indels
                          Length
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                           216;
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 37;
                                                                                                                                                                                                                                                    CDNAS
Gaps
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                         O35853;
O35853;
O1-JAN-1998
O1-JAN-1998
O1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF307013; NON_TER 1 217 SEQUENCE 217 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herbst M.M., Schountz T.;
Herbst M.M., Schountz T.;
"Cloning of the deer mouse interferon gamma, necrosis factor genes.";
Submitted (SEP-2000) to the EMBL/GenBank/DDB.
EMBL; AF307013; AAG30264.1; -.
                                                                                                          01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2001 (TrEMBLrel. 16,
TUMOR NECROSIS FACTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).
Peromyscus maniculatus (Deer mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ERG6;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
                                                                                                  TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ERG6
MEDLINE=97246744; PubMed=9089109;
              SEQUENCE FROM STRAIN-A/J;
                                                 NCBI_TaxID=10090;
                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peromyscus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUÉ≃SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 130
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                                                                                                                                                                                                                                       VNLLSAIKSPC-PKETPEGSELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLD
                                                                                                                                                                                                                                                               ILLMKSARNSCWSKDAEYG------LYSIYQGGIFELKENDRIFVSVTNEHLID 177
                                                                                                                                                                                                                                                                                                                 HSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 129
                                                                                                                                                                                                                                                                                                                                                                   ISPLVRERGPQRVAAHITGTRGRSNTL-SSPNSKNEKALGRKINS-----WESSRSG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVNLLSAIKSPC-PKETPEGEELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMSLKDNQLVIPADGLYLVYSQVLFRGQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPQRVAAH---ITGTRGRSNTL-SSPNSKNEKALGRKINS--------WESSRSGHSFLS
                                                                                                                                                                                                                                                                                        ALLANGMDLKDNQLVIPADGLYLVYSQVLFKGQ-----GCSNYVLLTHTVSRFAVSYEDK
                                                                                                                                                                                                                                                                                                                                          IGPOREEKFPNNLP--IIGSMAQTLTLRSSSQNSSDKPVAHVVANHQVDEQLEWLSRRAN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK-----YTSYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPQREEKFPNPIIGSMGQTLTLRSSSQNSNDKPVGHVVANHQVEEQLEWLSHRANALLAN
                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                     (Mouse)
                        N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                           217
23964 MW; · D6F90C74C0B3021F CRC64;
                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                         13.6%;
                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                         Last sequence up
                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                      Score 135; DB 11;
Pred. No. 0.00017;
                                                           Craniata; Ver
Sciurognathi;
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217
                                                             Vertebrata;
thi; Muridae;
                                                                                                                                                                            A
                                                                                                                                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                            72;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                            Euteleostomi; 
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                     217;
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Best Local S
Matches 41
                                                                                                  Matches
                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       Q9IB42;
Q1-QCT-2000 (TrEMBLrel. 15, Createq)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TUMOR NECROSIS FACTOR.
Paralichthys olivaceus (Flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Acanthomorpha; Bothidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9IB42;
Q9IB42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01234; TNECROSISFCT PRODOR; PD002011; -; 1. PROSITE; PS00251; TNE_1; 1. PROSITE; PS50049; TNF_2; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                  PRINTS; PR01234; TNECROSISFCT.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 225 AA; 24965 MW;
                                                                                                                                                                                                          Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB040448; BAA94969.1; -.
InterPro; IPR000478; -.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000478; -.
InterPro; IPR003636; -.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                     olivaceus."
                                                                                                                                                                                                                                                                        factor (TNF) cDNA and gene from Japanese plivaceus ".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U68414; AAB65593.1;
HSSP; P06804; 2TNF.
                                                                                                                                                                                                                                                                                              irono I., Nam B., Kurobe T., Aoki T.;
Molecular cloning, characterization a
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iraqi F., Teale A.;
"Cloning and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 45:459-461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 VKSPC-PKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
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                                                           EKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG
                SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ-----
                                          EKTEPHNTLRQISSRAKAAIHLEG-RDEEDEETSENKLVWKNDEGLA-----FTQGGF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPQRDEKFPNGLPLISSMAQTLSSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANG 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDLKDNQLVVPADGLYLVYSQVLFKGQ-----GCPDYVLLTHTVSRFAISYQEKVNLLSA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 AA;
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                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                              12.7%;
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23.0%;
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                                                                                                              Score 126.5; DB Pred. No. 0.001;
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Pred. No. 0.00038;
5; Mismatches 77;
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                                                                                                                                                                     8F947FB25FC82658 CRC64;
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                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                 expression of tumor necrosis flounder Paralichthys
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-EEIKENTKNDKQMVQY-IYKYT 124
                                                                                                                           DB 13;
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                                                                                                Gaps
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Search completed: October Job time: 109 sec

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Best Local Similarity
Matches 43; Conser
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Q9UKS8;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                       PRINTS; PR01234; TNECROSISFCT.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
SMARP; SM00207; TNF; 1.
VARIANT 1
                                                                                                                                                                                                                                                                                                                                                                                                                        Rowen L., Madan A.,
Abbasi N., Dickhoff
Lasky S., Hood L.;
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000478; -
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYMPHOTOXIN ALPHA.
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            EMBL; AF129756; AAI
HSSP; P01375; 4TSV
                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                region."
                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
 193
                       178
                                                 135
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                      MDHEASFFGAF 188
                                                                                                                                                                     TISTVQEKQQ------NISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGR
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LSPSTVFFGAF
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                                                                       IYKYTS-YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN-EHLID 177
                                                                                                                       KINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQY 119
                                                                                                                                                 TPSAAQTARQHPKMHLAHSNLKP-----AAHLIGDPSKQNSL---
                                                                                               ---LWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYSPKATSSPLYLAHE
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amphotropic murine
                                                                                                    lymphotoxin beta -
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ALIGNMENTS

RESULT 1 A53062 Fas ligand - mouse

C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.;
Cell 76, 969-976, 194
A;Title: Generalized 194
A;Title: Generalized 19mphoproliferative disease in mice, caused by a point mutation A;Reference number: A53062; MUID:94185175
A;Accession: A53062

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-279 <TAK>

A;Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

HEOUDRHEGEGE	מ ט ט	0 0		0	••
I38707 Fas ligand - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000 C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000 C;Accession: I38707, JC2340; S57565; I38554 R;Takahashi, T; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S. Int. Immunol. 6, 1567-1574, 1994 A;Title: Human Fas ligand: gene structure, chromosomal location and species specifici A;Reference number: I38707; MUID:95127560 A;Reference number: I38707; MUID:95127560 A;Accession: I38707 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-281 <res></res>	Qy 188 F 188 Db 277 Y 277 RESULT 2	129 PILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGA 	Db 122 VSSFEKQIANPSTPSEKKEPRSV-AHLTGNPHSRSIPLEWEDT-Y 164 Qy 70 GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYPD 128 : :	Matches 49; Conservative 46; Mismatches 59; Indels 27; Gaps 8; OY 10 ISTVQEKQQNISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS 69 : : ::: :: :: : : : :	Query Match 18.9%; Score 188.5; DB 2; Length 279; Best Local Similarity 27.1%; Pred. No. 2.4e-09;

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C >
                                                                                                                 C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Naga Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of A;Reference number: A49266; MUID:94084792
A;Accession: A49266
                                                                                                                                                                                                                                                                                                                                    RESULT
A49266
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C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <
F;76,184,250,260/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.;
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731
A;Accession: I38554
                                               A; Molecule type: mRNA
A; Residues: 1-278 <SUD>
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                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05:Nov-1999
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A; Residues: 1-281 <RE2>
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A; Residues: 1-281 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1;
Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Gene: FasL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRESTSQMHTASSLEKQIGHPSP-PPEKKELRKVAHLT---GKSNSRSMP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHLIDMDHEASFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LEWEDT-YGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IY-KYTSYPDPILLMKSARNS-----CWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-281 <MIT>
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                        PID:g440179
                                                                                                                                                                   novel member of the
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cytotoxin;

glycoprotein;

lymphokine;

macrophage

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A; Introns: 32/3; 68/1 C; Superfamily: tumor of C; Keywords: cytokine;
                                               A; Cross-references: EMBL: X54859; NID: g2132; C; Genetics:
                                                                               A; Molecule type: DNA
A; Residues: 1-204 < KUH>
                                                                                                               A; Reference number: S17289;
A; Accession: S17289
                                                                                                                                                                Gene 102,
                                                                                                                                                                                             tumor necrosis factor beta precursor - pig
c;Species: Sus scrofa domestica (domestic plg)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S17289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD40 ligand - bovine
C;Species: Bos primitgenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-
C;Accession: $53090
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                                                                                                                                               A; Title: The porcine tumor necrosis factor-encoding
                                                                                                                                                                R; Kuhnert, P.; Wuethrich, Gene 102, 171-178, 1991
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A; Residues: 1-261 <MER>
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                                                                                                                                                                                                                                                                                                                                                                                                                            FLSN--LHLRNG-ELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKKKEKNFEMHKGDQEPQ-IAAHV--
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Ly: tumor necrosis
cytokine; cytotoxi
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                                                                                                                                                                              C.; Peterhans,
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                                                                                                                              MUID:91340150
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                  factor
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Pred. No. 2.9e
33; Mismatches
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Pred. No. 2.2
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                                                                                                                                                                                 E.; Pauli,
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                                                                 PIDN:CAA38638.1;
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                                                                                                                                               sequence and comparative
                                                                PID:g2133
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Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF
A;Reference number: JH0309; MUID:91065534
A;Accession: JS0727
A;Accession: JS0727
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Ş
                                                                                                                                    F;83/Binding site: c
F;147-178/Disulfide
                                                                                                                                                                                       C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymp
F;1-81/Domain: propeptide #status predicted <PRO>
F;82-234/Product: tumor necrosis factor #status predicted <MAT>
                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-62, 'Q', 63-234 <SHA>
A; Cross-references: GB: M60340; GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: this sequence differs from that shown R; Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Gene 95, 215-221, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor A;Reference number: A25451; MUID:86219712
A;Accession: A25451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M12845; NID:g165759; R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Molecular cloning a A; Reference number: A25454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Ito, H.; Yamamoto, DNA 5, 149-156, 1986
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                                                                                                                                                                                                                                                                                                                                                                  A; Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-234 <IT2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-234 <ITO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A25454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                     ;19,20/Binding site: myristate (Lys) (covalent) #status ;83/Binding site: carbohydrate (Ser) (covalent) #status
                                                                                                                                                                                                                                                                                             ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                        Query Match
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                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 VFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 SFFGAF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157-165, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 STVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 46; Conserv
  28 GPQRVAA----HITGTRGRSNTL-SSPNSKNEKALGRKINS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSQYPFHVPLLSAQKSVCPGPQGPW-VRSVYQGAVFLLTQGDQLSTHTDGTPHLLLSPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TS-YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAAQPAHQH-PPKHLARGTLKPAAHLVGDPSTPDSLRWRANT-----DRAFLR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----HGFL----LSNNSLLVPTSGLYFVYSQVVFSGEGCFPKATPTPLYLAHEVQLF 137
                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
                                                                                                                                                                                                                                                                         80/1; 96/1
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                                                                                                                                      bonds:
                                                        13.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and expression; MUID:86219711
                                                                                                                                    #status predicted
                                                                                                                                                                                                                                                                                                              GB:M35326;
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Pred. No. 0.0001;
Pred. No. 76;
                                      Score 130.5; DB 1;
Pred. No. 0.00027;
6; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                      shown;
                                                                                                                                                                                                                                                                                                            NID:g165754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in Escherichia coli of the
                                                                                                                                                                                                                                                                                                                                                                      translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:AAA31486.1; M.; Kawahara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in having a Gln inserted between Jongeneel, C.V.; Nedospasov, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              locus,
                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kajihara,
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                                                                                                                                                                                                                                                                                                                                                                                                                            containing the
                                                                                                                                                                                                                                                                                                            PIDN: AAA31484.1;
                                                                        Length
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                                        Indels
  ----WESSRSGHSFL 74
                                                                                                                                                     predicted
predicted
                                                                                                                                                                                                                                 lymphokine;
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; Todd, C.W.; Wallace,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204;
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                                        25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                   macrophage;
                                                                                                                                                                                                                                                                                                            PID:g165756
                                                                                                                                                                                                                                                                                                                                                                                                                            encoding
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                                      7;
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C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokin F;1-77/Domain: propeptide #status predicted <PRO> F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT> F;19,20/Binding site: myristate (Lys) (covalent) #status predicted F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted F;144-176/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Pauli, V., T., 1989
Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-232 < KUH>
A; Cross-references: EMBL: x54859; NID: g2132; PIDN: CAA38639.1;
A; Cross-references: EMBL: x54859; NID: g2132; PIDN: CAA38639.1;
A; Note: the authors translated the codon GAG for residue 202
R; Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: S12066; S17290; S18965; 146659
R;Drews, R.T.: Coffee P. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 44-232 <PAU>
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A; Accession: I46659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative A; Reference number: $17289; MUID: $91340150 A; Accession: $17290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X54001; NID:g2135; | R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Gene 102, 171-178, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; Mcc
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 62/3; 78/1; 93/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; R;Pauli, U.; Beutler, B.; Peterhans, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-232 <CHO>
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                                                                                                                                                                                          Query Match
Best Local
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                                                          66
                                                                                                            28
VIHEKGFYYIYSQTYFRFQEEIKEN---TKNDKQMVQYIYKYTSYPDPILLMKSARNSCW
                                                       GPLSINPLAQGLRSSSQTSDKPVAHVVANVKAEGQL--QWQSGYANALLANGVKLKDNQL 123
                                                                                                         GPQRVAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHLRNGEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDPILLM 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor necrosis factor
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:M29079; NID:g164694; PIDN:AAA31128.1;
                                                                                                                                                                                          13.1%;
                                                                                                                                                                 30;
                                                                                                                                                              Score 130; DB 1;
Pred. No. 0.00029
0; Mismatches 7
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a
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as Gly
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                                                                                                                                                              Gaps
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C:Keywords: glycoprotein; transmembrane protein F;23-46/Domain: transmembrane #status predicted <TMM>F;47-260/Domain: extracellular #status predicted <EXTF F;47-260/Domain extracellular #status predicted <EXTF F;239/Binding site: carbohydrate (Asn) (covalent) #st
                                                                                                                                R;Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, Cosman, D.; Spriggs, M.K.
Nature 357, 80-82, 1992
A;Title: Molecular and biological characterization of A;Reference number: S21738; MUID:92244364
A;Accession: S21738
                                                                                                                                                                                                                                      C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
C:Accession: S21738
                                                                                                                                                                                                                                                                                                                                RESULT
S21738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: PITNF
A;Gene: PITNF
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Superfamily: timor necrosis factor
C;Reywords: glycoprotein; lipoprotein; myristylation
C;Reywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status
F;84/Binding site: carbohydrate (Ser) (covalent) #status
                                                                                        A; Molecule type: mRNA
A; Residues: 1-260 <ARM>
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C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000 C;Accession: I54490
                                                                          A;Cross-references: EMBL:X65453; NID:g50351; PIDN:CAA46448.1;
                                                                                                                                                                                                                                                                                                                CD40 ligand
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Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin
A;Reference number: I54490; MUID:92218012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-235 < R
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Best Local s
Matches 45
                                                                                                                                                                                                                                                                                                                                                                                                            228
                                                                                                                                                                                                                                                                                                                                                                                                                                                184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72
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                                                                                                                                                                                                                                                                                                                                                                                                            VYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -FFG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILLMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLANGMDLKDNQLVIPADGLYLVYSQVLFKGQ-----GCSSYVLLTHTVSRFAVSYEDK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RETPEGAEAKPWYEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQVYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SK-----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNLLSAIKSPC-PKETPEGSELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGPQREEKFPNNLP--IIGSMAQTLTLRSSSQNSSDKPVAHVVANHQVDEQLEWLSRGAN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISPLVRERGPORVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSGH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVPTDGLYLIYSQVLFRGQGCPSTNVFLTHTISRIA-----VSYQTKVNLLSAIKSPCQ
                                                                                                                                                                                                                                                                                                                - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
45; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
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24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 129.5; DB 2;
Pred. No. 0.00033;
9; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from GB/EMBL/DDBJ
predicted <EXT>
(covalent) #status
                                                                                                                                                                                                                                  Sato,
                                                                                                                                                                        a murine ligand for CD40
                                                                                                                                                                                                                                T.A.; Clifford, K.N.; Macduff, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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predicted
predicted
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                                                                          PID:g50352
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Gene 107, 319-321, 1991

A;Title: Cloning and characterization of gene A;Title: Cloning Type 201344; MUID:92084125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I46046; S24641
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
Cytokine 5, 336-341, 1993
Cytokine 5, 336-341, 1993
Cytokine 5, 336-341, 1993
Cytokine 5, 36-341, 1993
Cyto
                                      A; Molecule type: DNA
A; Residues: 1-234 <SUX>
                                                                                                           A; Reference number: JQ1344; A; Accession: JQ1344
                                                                                                                                                                                                                                                                                                                                   C;Species: Equus caballus (domestic hor C;Date: 10-Sep-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor alpha precursor N;Alternate names: cachectin; TNF alpha C;Species: Equus caballus (domestic horses)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 32/3; 68/1 C; Superfamily: tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-204 <CL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: I46046; A; Accession: I46046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDB:
       A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lymphotoxin
                                                                                                                                                                                                                                                                                            Accession: JQ1344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 HEASFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 KYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTN-EHLIDMD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 ---QW-AKKGYYTMKSNLVMLENGKQLTVKREGLYYVYTQVTFCSNRE----PSSQRPFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 NSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSSVFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFSPQYPFHVPLLSAQKSVCPGPQGPW-VRSVYQGAVFLLTRGDQLSTHTDGISHLL-LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPSAAQPAHQQL-PTPFTRGTLKPAAHLVGDPSTQDSLRWRANT-----DRAFLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISTVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KINSWESSRSGHSFLSNL-HLRNG-ELVIHEKGFYYYYSQTYFRFQEEIKENTKNDKQMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGLWLKPSIGSERILLKAANTHSSSQLCEQ--QSVHLGGVFELQAGASVFVNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HGF----SLSNNSLLVPTSGLYFVYSQVVFSGRGCFPRATPTPLYLAHEVQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RQFEDLVKDITLNKEEKKENSFEMQRGDEDPQIAAHV-----VSEANSNAASVL-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47;

    bovine

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188
   GB:M64087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: 214137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       necrosis factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.9%;
25.3%;
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NID: g164244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 127.5; DB 1 Pred. No. 0.00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.005; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 128.5; DB 2
Pred. No. 0.00046;
                                                                                                                                                                                                                                                                                                                                                                             horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                   10-sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   horse
   PIDN: AAA30959.1;
                                                                                                                                                                                        TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                        alpha
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                                                                                                                                                                                                                                                                                                                                       #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arranged bovine lymphotoxin and
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                                                                                                                                                                                 encoding equine tumor necros:
PID:g164245
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C;Comment: This protein is an important proximal mediator of endotoxemia.
C;Genetics:
A;Genetics:
A;Ge
              A;Reference number: S26694; MUID:93076854
A;Accession: S26694
A;Status:
                                                                                                   A;Experimental source: peripheral blood T-cell
R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek,
Eur. J. Immunol. 22, 3191-3194, 1992
A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.
                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:215017; NID:938483; PIDN:CAA78737.1; PID:938484 R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, J. Exp. Med. 176, 1543-1550, 1992 A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and Reference number: JH0793; MUID:93094757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The human T cell antigen gp39, a A;Reference number: $28017; MUID:93049181 A;Accession: $28017
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C;Accession: I53476; S28017; JH0793; S26694; S28852; S25684; S30593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 315, 259-266, 1992
A;Title: Human CD40-ligand: Molecular cloning,
A;Reference number: I53476; MUID:93138085
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                                                                                                                                                                                                                                              A;Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1;
                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-261 <SPR>
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Status: preliminary
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A;Title: Dense Alu clustering and a potential A;Reference number: S36152; MUID:93272029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; AR;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Nucleic Acids Res. 13, 6361-6373, 1985
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                                                                                                      R; Pennica, D.; Nedwin, G. Nature 312, 724-729, 1984
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   A; Accession:
                             A; Title: Human tumour necrosis factor: precursor A; Reference number: A93351; MUID: 85086244
                                                                                                                                    A; Note: the nucleotide sequence was submitted R; Pennica, D.; Nedwin, G.E.; Hayflick, J.S.;
                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-233 <IRI>
                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: S36153
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A; Residues: 1-233 <NED>
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A; Residues: 1-261 <GAU>
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not

shown;

translation

not shown

l to the EMBL Data Library, i Seeburg, P.H.; Derynck, R.;

August 1992

Palladino, homology

3

structure,

expression

and

NID: g37209; PIDN: CAA26669.1;

PID: 937210

homology and

A01646;

Caterina, new member of

D.;

the

NFkappaB

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A;Map position: Xq26-Xq26
C;Keywords: alvannia
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Reywords: glycoprotein: transmembrane protein F;13-44/Domain: transmembrane #status predicted F;45-261/Domain: extracellular #status predictec F;6,240/Binding site: carbohydrate (Asn) (covale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:CD40LG; HIGM1; IMD3
A;Cross-references: GDB:120632; OMIM:308230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jome FEBS Lett. 315, 259-266, 1993 A;Title: Human CD40-ligand: molecular cloning, cellular A;Reference number: S28852; MUID:93138085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-261 <GRA>
A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1 200
A; Cross-references: EMBL: L07414;
Note: the sequence from Fig. 3
171 TNEHLIDMDHEASFFG
                                                                                        111 KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 170
                                                                                                                                              -QW--AEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCL 195
                                                                                                                                                                                           NSWESSRSGHSFLSN--LHLRNG-ELVIHEKGFYYIYSQTYFRFQEEIKENT-----
                                                                                                                                                                                                                                                                                         ILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKI
                                                                                                                                                                                                                                              IMLNKEET----KKENSFEMQKGDQNPQ-IAAHV-----ISEASSKTTSVL----
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                12.5%;
186
                                             ----ILLRAANTHSSAKPC--GQQSIHLGGVFELQPGASVFVNV
                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID:g180123; PIDN:AAA35662.1; PID:g180124 is inconsistent with that from Fig. 2 in having
                                                                                                                                                                                                                                                                                                                                                                Score 124.5; DB Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted
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T.; Elson, (
                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                       Gaps
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C; Keywords: Cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; F;1-76/Domain: propeptide #status predicted FRO
F;71-76/Domain: propeptide #status experimental cMAT
F;77-233/Product: tumor necrosis factor #status experimental cMAT
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental files for the covalent of the covalent 
                                                                                                                                                                                                                                                                                A:Gene: GDB:TNF; TNFA
A:Cross-references: GDB:120441; OMIM
A:Map position: 6p21.3-6p21.3
A:Introns: 62/3; 78/1; 94/1
C:Complex: homotrimer
C:Superfamily: tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction out detriment to normal cells. It can also act synergistically with interferon gamma to C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely ut are produced by different cell types and have different induction kinetics.
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J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha partitle: Myristyl acylation of the tumor necrosis factor alpha partitle: Association of myristylated lysines A;Contents: annotation; identification of myristylated lysines R;AggarWal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S;Biol. Chem. 260, 2345-2354, 1985
J. Biol. Chem. 260, 2345-2354, 1985
J. Title: Human tumor necrosis factor. Production, purification, A;Reference number: A92511; MUID:85130974
A;Contents: annotation; disulfide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Molecule type: protein
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Blochem. 152, 515-522, 1985
A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A;Reference number: I53311; MUID:86030296
A;Accession: I53311
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Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type; DNA
A; Residues: 1-23 <MAR>
A; Residues: 1-23 <MAR>
A; Cross-references: GB:M26331; NID:g339763;
A; Experimental source: U-937 cells
A; Experimental source: U-937 cells
R; Takakura-Yamamoto, R; Yamamoto, S; Fukud
Eur. J. Blochem. 235, 431-437, 196
B; Title: O-Glycosylated species of natural h
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A; Title: Simultaneous production of natural
A; Reference number: A61478; MUID:88301617
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A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyel R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Science 228, 149-154, 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-8 < DAL>
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A; Residues: 1-62, 'S', 64-233 <WAN>
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     /Disulfide
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A)Cross references: GB:X01393; NID:g34444; PIDN:CAA25649.1
A;Experimental source: lymphoblastoid cell line RPMI-1788
R;Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.;
Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A;Title: Tumor necrosis factors: gene structure and biolog
A;Reference number: A32877; MUID:87217059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-12, 'R', 14-205 < IRI>
A;Residues: 1-12, 'R', 14-205 < IRI>
A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78746.1; PID:g37213
A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78746.1; PID:g37213
A;Coss-references: EMBL:Z15026; NID:g37211; PIDN:CAA78746.1; PID:g37213
A;Coss-reference value sequence was submitted to the EMBL Data Library, F
R;Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991
A;Title: Haplotypic polymorphisms of the TNFB gene.
A;Reference number: I54482; MUID:93139175
A;Accession: I54482
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000 C;Accession: A92755; S36154; I54482; A93350; B32877; A91906; A61478; S26951; R;Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A
                                                                                                                                                                                                                                                                                                                                                           R;Gray, P.W.; Aggarwal, B
Nature 312, 721-724, 1984
                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-124, 'P', 126-205 <RES>
A; Residues: 1-124, 'P', 126-205 <RES>
A; Cross-references: GB:M55913; NID:g339742; PIDN:AAB59455.1;
A; Experimental source: ancestral haplotype 57.1
A; Note: 59-Asn was also found (ancestral haplotype 8.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Dense Alu clustering and a potential A;Reference number: S36152; MOID:93272029 A;Accession: S36154 A;Status: nucleic acid sequence not shown; tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-59,'N',61-205 <NED>
R; Iris, F.J.M.; Bougueleret, L.; I
Rature Genet. 3, 137-145, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphotoxin alpha precursor - huma
N;Alternate names: lymphotoxin A;
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
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                                                                     A; Reference number: A; Accession: B32877
                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-205 <GRA>
                                                                                                                                                                                                                                                                                       A;Reference number: A93350; MUID:85086243
A;Accession: A93350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, J. Cell. Biochem. 29, 171-181, 1985
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                                            A;Status:
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                                                                                                                                                                                                                                                                                                                                       A; Title: Cloning and expression of cDNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                            preliminary; not
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type: ml
: 35-205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bougueleret, L.; Prieur, 137-145, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229
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                                                                                                                                                                                                                                                                                                                                                                                    B.B.; Benton, C.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.3%;
                                               compared with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNF beta; tumor necrosis factor beta (TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              localization
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                                               conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.; Caterina, D.; Primas,
                                                                                                                                                                                      PIDN:CAA25649.1; PID:g34445
line RPMI-1788
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                                                                                                                                                                                                                                                                                                                                       human lymphotoxin,
                                                                                                                                                                                                                                                                                                                                                                                 Bringman,
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                                                                                                                                                                                                                                                                                                                                                                                 T.S.; Henzel, W.J.; Jarrett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                  Nedwin, G.E.; Palladino,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID: 9339743
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                                                                                                                                                                                                                                                                                                                                       lymphokine
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Y.; Goedd
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A;Note: the first intron occurs before the initiator codon C;Superfamily: tumor necrosis factor C;Superfamily: tumor necrosis factor C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphoki F;1-34/Domain: signal sequence #status predicted <SIG> F;35-205/Product: lymphotoxin #status predicted <MAT> F;41/Binding site: carbohydrate (Thr) (covalent) #status experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: 60-Thr was also found R;Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, Arch. Biochem. Biophys. 304, 144-153, 1993
A;Title: N-linked sugar chain structure of recombinant human A;Reference number: S34742; MUID:93311995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 56-79;86-95,'X',97,'X',99;119-151,'XX',154-162,'X',164,'X',166,'X',168,'X'
R; Voigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.
FEBS Lett. 314, 85-88, 1992
A; Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylat
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A:Residues: 1-59, NY,61-205 <KOB>
A:Residues: 1-59, NY,61-205 <KOB>
A:Residues: 1-59, NY,61-205 <KOB>
A:Ross-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914
A:ROte: the authors translated the codon TAT for residue 156 as Thr and a:R:Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Na:Lymphokine Res. 7, 175-185, 1988
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J. Biochem. 100, 727-733, 1986
A;Title: Cloning and expression of human
A;Reference number: A91906; MUID:87057135
A;Accession: A91906
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A; Reference number:
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                          R;Shirai,
                                                                                                                           tumor necrosis factor alpha po
N; Alternate names: cachectin;
                                                                                                                                                                                                                                                                                     B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       while having no detrimental effect on normal cells. It can also act synergistically with comment: This protein and TNF-alpha (tumor necrosis factor) are the products of different activities but are produced by different cell types and have different induction kardinary.
                     ;Species: Mus musculus (house mouse)
;Species: Mus musculus (house mouse)
;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000;
;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000;
;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696;
;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: GDB:LTA; LT; TNFB
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                  167 MYHGAAFQLTQGDQLSTHTDGIPHLV-LSPSTVFFGAF
                                                                                                                                                                                                                                                                                                                                     152
193-201,
                                                                                                                                                                                                                                                                                                                                                                                                                                            93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY 92
                                                                                                                                                                                                                                                                                                                                   IYQGGIFELKENDRIFVSVTN-EHLIDMDHEASFFGAF
                                                                                                                                                                                                                                                                                                                                                                                         FVYSQVVFSGKAYSPKATSSPLYLAHEVQLFSSQYPFHVPLL-SSQKMVYPGLQEPWLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                         YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTS-YPDPILLMKSARNSCWSKDAEYGLYS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted from mitogen-activated lymphocytes within 1-2 days after induction,
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37; Conserv
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                                                                                                                           precursor -
n; TNF alpha
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Pred. No. 0.
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                                                                                                                                                      mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.0013;
72;
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C; Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; F;80-235/Product: tumor necrosis factor #status experimental cMAT>
F;20/Binding site: myristate (Lys) (covalent) #status predicted F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
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J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor
A;Reference number: A34251; MUID:89380231
A;Accession: A34251
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Nucleic Acids Res. 13, 4417-4429, 1985
A:Title: Molecular cloning of mouse tumour
A:Reference number: A23127; MUID:85242112
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A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087
A;Note: article in Russian with English abstract
A;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, Nucleic Acids Res. 15, 9083-9084, 1987
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A;Residues: 1-230,'R', 232-235 <RES>
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A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1;
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
R;Sherry, B.; Jue, D.M.; Zentella, A.; 1072-1078. 1990
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A; Residues: 1-235 <FRA>
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A;Title: Cloning and expression in Escherichia coli of the cDNA
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                                                                                                                                           C; Superfamily: tumor necrosis factor
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                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 80-85, 'X', 87-99
                                                                                                                                                                                                                                                                                                                              A; Reference number: A36696; MUID: 91097531
                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 173, 1072-107
A; Title: Characterization of high molecular
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A; Residues: 1-235 <PEN>
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A; Residues: 1-235 <S
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A; Residues: 1-23
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